



APR 24 2002

-90-

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Daggett, Lorrie P.
Ellis, Steven B.
Liaw, Chen W.
Lu, Chin-Chun

(ii) TITLE OF INVENTION: HUMAN N-METHYL-D-ASPARTATE RECEPTOR
SUBUNITS, NUCLEIC ACIDS ENCODING SAME AND USES THEREFOR

(iii) NUMBER OF SEQUENCES: 63

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Brown, Martin, Haller & McClain
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(C) CITY: San Diego
(D) STATE: CA
(E) COUNTRY: U.S.A.
(F) ZIP: 92101-2926

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE: 29-SEPT-97
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/231,193
(B) FILING DATE: 20-APR-1994
(C) CLASSIFICATION:

(viii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/052,449
(B) FILING DATE: 20-APR-1993
(C) CLASSIFICATION:

(ix) ATTORNEY/AGENT INFORMATION:

(A) NAME: Seidman, Stephanie
(B) REGISTRATION NUMBER: 33,779
(C) REFERENCE/DOCKET NUMBER: 6362-9383C

(x) TELECOMMUNICATION INFORMATION:

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 4298 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME /KEY: CDS
(B) LOCATION: 262..3078

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CAAGCCGGGC GTTCGGAGCT GTGCCGGCC CGCCTTCAGC ACCGCGGACA GCGCCGGCCG	60
CGTGGGGCTG AGCGCCGAGC CCCCGCGCAC GCTTCAGCCC CCCTTCCTC GGCGACGTC	120
CCGGGACCGC CGCTCCGGGG GAGACGTGGC GTCCGCAGCC CGCGGGGCCG GGCGAGCGCA	180
GGACGGCCCCG GAAGCCCCGC GGGGGATGCG CCGAGGGCCC CGCGTTCGCG CGCGCAGAG	240
CCAGGGCCCGC GGCCCGAGCC C ATG AGC ACC ATG CGC CTG CTG ACG CTC GCC	291
Met Ser Thr Met Arg Leu Leu Thr Leu Ala	
1 5 10	
CTG CTG TTC TCC TGC TCC GCC CGT GCC GCG TGC GAC CCC AAG ATC	339
Leu Leu Phe Ser Cys Ser Val Ala Arg Ala Ala Cys Asp Pro Lys Ile	
15 20 25	
GTC AAC ATT GGC GCG GTG CTG AGC ACG CGG AAG CAC GAG CAG ATG TTC	387
Val Asn Ile Gly Ala Val Leu Ser Thr Arg Lys His Glu Gln Met Phe	
30 35 40	
CGC GAG GCC GTG AAC CAG GCC AAC AAG CGG CAC GGC TCC TGG AAG ATT	435
Arg Glu Ala Val Asn Gln Ala Asn Lys Arg His Gly Ser Trp Lys Ile	
45 50 55	
CAG CTC AAT GCC ACC TCC GTC ACG CAC AAG CCC AAC GCC ATC CAG ATG	483
Gln Leu Asn Ala Thr Ser Val Thr His Lys Pro Asn Ala Ile Gln Met	
60 65 70	
GCT CTG TCG GTG TGC GAG GAC CTC ATC TCC AGC CAG GTC TAC GCC ATC	531
Ala Leu Ser Val Cys Glu Asp Leu Ile Ser Ser Gln Val Tyr Ala Ile	
75 80 85 90	
CTA GTT AGC CAT CCA CCT ACC CCC AAC GAC CAC TTC ACT CCC ACC CCT	579
Leu Val Ser His Pro Pro Thr Pro Asn Asp His Phe Thr Pro Thr Pro	
95 100 105	
GTC TCC TAC ACA GCC GGC TTC TAC CGC ATA CCC GTG CTG GGG CTG ACC	627
Val Ser Tyr Ala Gly Phe Tyr Arg Ile Pro Val Leu Gly Leu Thr	
110 115 120	
ACC CGC ATG TCC ATC TAC TCG GAC AAG AGC ATC CAC CTG AGC TTC CTG	675
Thr Arg Met Ser Ile Tyr Ser Asp Lys Ser Ile His Leu Ser Phe Leu	
125 130 135	
CGC ACC GTG CCG CCC TAC TCC CAC CAG TCC AGC GTG TGG TTT GAG ATG	723
Arg Thr Val Pro Pro Tyr Ser His Gln Ser Ser Val Trp Phe Glu Met	
140 145 150	
ATG CGT GTC TAC AGC TGG AAC CAC ATC ATC CTG CTG GTC AGC GAC GAC	771
Met Arg Val Tyr Ser Trp Asn His Ile Ile Leu Leu Val Ser Asp Asp	
155 160 165 170	
CAC GAG GGC CGG GCG GCT CAG AAA CGC CTG GAG ACG CTG CTG GAG GAG	819
His Glu Gly Arg Ala Ala Gln Lys Arg Leu Glu Thr Leu Leu Glu Glu	
175 180 185	
CGT GAG TCC AAG GCA GAG AAG GTG CTG CAG TTT GAC CCA GGG ACC AAG	867
Arg Glu Ser Lys Ala Glu Lys Val Leu Gln Phe Asp Pro Gly Thr Lys	
190 195 200	
AAC GTG ACG GCC CTG CTG ATG GAG GCG AAA GAG CTG GAG GGC CGG GTC	915
Asn Val Thr Ala Leu Leu Met Glu Ala Lys Glu Leu Glu Ala Arg Val	

205	210	215	
ATC ATC CTT TCT GCC AGC GAG GAC GAT GCT GCC ACT GTA TAC CGC GCA Ile Ile Leu Ser Ala Ser Glu Asp Asp Ala Ala Thr Val Tyr Arg Ala 220 225 230			963
GCC GCG ATG CTG AAC ATG ACG GGC TCC GGG TAC GTG TGG CTG GTC GGC Ala Ala Met Leu Asn Met Thr Gly Ser Gly Tyr Val Trp Leu Val GLY 235 240 245 250			1011
GAG CGC GAG ATC TCG GGG AAC GCC CTG CGC TAC GCC CCA GAC GGC ATC Glu Arg Glu Ile Ser Gly Asn Ala Leu Arg Tyr Ala Pro Asp Gly Ile 255 260 265			1059
CTC GG3 CTG CAG CTC ATC AAC GGC AAG AAC GAG TCG GCC CAC ATC AGC Leu Gly Leu Gln Leu Ile Asn Gly Lys Asn Glu Ser Ala His Ile Ser 270 275 280			1107
GAC GCC GTG GGC GTG GTG GCC CAG GCC GTG CAC GAG CTC CTC GAG AAG Asp Ala Val Gly Val Val Ala Gln Ala Val His Glu Leu Glu Lys 285 290 295			1155
GAG AAC ATC ACC GAC CCG CCG CGG GGC TGC GTG GGC AAC ACC AAC ATC Glu Asn Ile Thr Asp Pro Pro Arg Gly Cys Val Gly Asn Thr Asn Ile 300 305 310			1203
TGG AAG ACC GGG CCG CTC TTC AAG AGA GTG CTG ATG TCT TCC AAG TAT Trp Lys Thr Gly Pro Leu Phe Lys Arg Val Leu Met Ser Ser Lys Tyr 315 320 325 330			1251
GCG GAT GGG GTG ACT GGT CGC GTG GAG TTC AAT GAG GAT GGG GAC CGG Ala Asp Gly Val Thr Gly Arg Val Glu Phe Asn Glu Asp Gly Asp Arg 335 340 345			1299
AAG TTC GCC AAC TAC AGC ATC ATG AAC CTG CAG AAC CGC AAG CTG GTG Lys Phe Ala Asn Tyr Ser Ile Met Asn Leu Gln Asn Arg Lys Leu Val 350 355 360			1347
CAA GTG GGC ATC TAC AAT GGC ACC CAC GTC ATC CCT AAT GAC AGG AAG Gln Val Gly Ile Tyr Asn Gly Thr His Val Ile Pro Asn Asp Arg Lys 365 370 375			1395
ATC ATC TGG CCA GGC GGA GAG ACA GAG AAG CCT CGA GGG TAC CAG ATG Ile Ile Trp Pro Gly Gly Glu Thr Glu Lys Pro Arg Gly Tyr Gln Met 380 385 390			1443
TCC ACC AGA CTG AAG ATT GTG ACG ATC CAC CAG GAG CCC TTC GTG TAC Ser Thr Arg Leu Lys Ile Val Thr Ile His Gln Glu Pro Phe Val Tyr 395 400 405 410			1491
GTC AAG CCC ACG CTG AGT GAT GGG ACA TGC AAG GAG GAG TTC ACA GTC Val Lys Pro Thr Leu Ser Asp Gly Thr Cys Lys Glu Glu Phe Thr Val 415 420 425			1539
AAC GGC GAC CCA GTC AAG AAG GTG ATC TGC ACC GGG CCC AAC GAC ACG Asn Gly Asp Pro Val Lys Lys Val Ile Cys Thr Gly Pro Asn Asp Thr 430 435 440			1587
TGG CCG GGC AGC CCC CGC CAC ACG GTG CCT CAG TGT TGC TAC GGC TTT Ser Pro Gly Ser Pro Arg His Thr Val Pro Gln Cys Cys Tyr Gly Phe 445 450 455			1635
TGC ATC GAC CTG CTC ATC AAG CTG GCA CGG ACC ATG AAC TTC ACC TAC Cys Ile Asp Leu Leu Ile Lys Leu Ala Arg Thr Met Asn Phe Thr Tyr 460 465 470			1683

GAG GTG CAA CTG GTG GCA GAT GGC AAG TTC GGC ACA CAG GAG CGG GTG Glu Val His Leu Val Ala Asp Gly Lys Phe Gly Thr Glu Glu Arg Val 475 480 485 490	1731
AAC AAC ACC AAC AAG AAG GAG TGG AAT GGG ATG ATG GGC GAG CTG CTC Asn Asn Ser Asn Lys Lys Glu Trp Asn Gly Met Met Gly Glu Leu Leu 495 500 505	1779
AGC GGG CAA GCA GAC ATG ATC GTG GCG CCG CTA ACC ATA AAC AAC GAG Ser Gly Gln Ala Asp Met Ile Val Ala Pro Leu Thr Ile Asn Asn Glu 510 515 520	1827
CGC GCG CAG TAS ATC GAG TTT TCC AAG CCC TTC AAG TAC CAG GGC CTG Arg Ala Gln Tyr Ile Glu Phe Ser Lys Pro Phe Lys Tyr Gln Gly Leu 525 530 535	1875
ACT ATT CTG GTC AAG AAG GAG ATT CCC CGG AGC ACG CTG GAC TCG TTC Thr Ile Leu Val Lys Lys Glu Ile Pro Arg Ser Thr Leu Asp Ser Phe 540 545 550	1923
ATG CAG CCG TTG CAG AGC ACA CTG TGG CTG CTG GTG GGG CTG TCG GTG Met Gln Pro Phe Gln Ser Thr Leu Trp Leu Val Gly Leu Ser Val 555 560 565 570	1971
CAC GTG GTG GCC GTG ATG CTG TAC CTG CTG GAC CGC TTC AGC CCC TTC His Val Val Ala Val Met Leu Tyr Leu Leu Asp Arg Phe Ser Pro Phe 575 580 585	2019
GGC CGG TTC AAG GTG AAC AGC GAG GAG GAG GAG GAC GCA CTG ACC Gly Arg Phe Lys Val Asn Ser Glu Glu Glu Glu Asp Ala Leu Thr 590 595 600	2067
CTG TCC TCG GCC ATG TGG TTC TCC TGG GGC GTC CTG CTC AAC TCC GGC Leu Ser Ser Ala Met Trp Phe Ser Trp Gly Val Leu Leu Asn Ser Gly 605 610 615	2115
ATC GGG GAA GGC GCC CCC AGA AGC TTC TCA GCG CGC ATC CTG GGC ATG Ile Gly Glu Gly Ala Pro Arg Ser Phe Ser Ala Arg Ile Leu Gly Met 620 625 630	2163
GTG TGG GCC GGC TTT GCC ATG ATC ATC GTG GCC TCC TAC ACC GCC AAC Val Trp Ala Gly Phe Ala Met Ile Ile Val Ala Ser Tyr Thr Ala Asn 635 640 645 650	2211
CTG GCG GCC TTC CTG GTG CTG GAC CGG CCG GAG GAG CGC ATC ACG GGC Leu Ala Ala Phe Leu Val Leu Asp Arg Pro Glu Glu Arg Ile Thr Gly 655 660 665	2259
ATC AAC GAC CCT CGG CTG AGG AAC CCC TCG GAC AAG TTT ATC TAC GCC Ile Asn Asp Pro Arg Leu Arg Asn Pro Ser Asp Lys Phe Ile Tyr Ala 670 675 680	2307
ACG GTG AAG CAG AGC TCC GTG GAT ATC TAC TTC CGG CGC CAG GTG GAG Thr Val Lys Gln Ser Ser Val Asp Ile Tyr Phe Arg Arg Gln Val Glu 685 690 695	2355
CTG AGC ACC ATG TAC CGG CAT ATG GAG AAG CAC AAC TAC GAG AGT GCG Leu Ser Thr Met Tyr Arg His Met Glu Lys His Asn Tyr Glu Ser Ala 700 705 710	2403
GCG GAG GCC ATC CAG GCC GTG AGA GAC AAC AAG CTG CAT GCC TTC ATC Ala Glu Ala Ile Gln Ala Val Arg Asp Asn Lys Leu His Ala Phe Ile 715 720 725 730	2451
TGG GAC TCG GCG GTG CTG GAG TTC GAG GCC TCG CAG AAG TGC GAC CTG Trp Asp Ser Ala Val Leu Glu Phe Glu Ala Ser Gln Lys Cys Asp Leu 735 740 745	2499

GTG ACG ACT GGA GAG CTG TTT TTC CGC TCG GGC TTC GGC ATA GGC ATG Val Thr Thr Gly Glu Leu Phe Phe Arg Ser Gly Phe Gly Ile Gly Met 750 755 760	2647
CGC AAA GAC AGC CCT TGG AAG CAG AAC GTC TCC CTG TCC ATC CTC AAG Arg Lys Asp Ser Pro Trp Lys Gln Asn Val Ser Leu Ser Ile Leu Lys 765 770 775	2696
TCC CAC GAG AAT GGC TTC ATG GAA GAC CTG GAC AAG ACG TGG GTT CGG Ser His Glu Asn Gly Phe Met Glu Asp Leu Asp Lys Thr Trp Val Arg 780 785 790	2643
TAT CAG GAA TGT GAC TCG CGC AGC AAC GCC CCT GCG ACC CTT ACT TTT Tyr Gln Glu Cys Asp Ser Arg Ser Asn Ala Pro Ala Thr Leu Thr Phe 795 800 805 810	2691
GAG AAC ATG GCC GGG GTC TTC ATG CTG GTA GCT GGG GGC ATC GTG GCC Glu Asn Met Ala Gly Val Phe Met Leu Val Ala Gly Gly Ile Val Ala 815 820 825	2739
GGG ATC TTC CTG ATT TTC ATC GAG ATT GCC TAC AAG CGG CAC AAG GAT Gly Ile Phe Leu Ile Phe Glu Ile Ala Tyr Lys Arg His Lys Asp 830 835 840	2787
GCT CGC CGG AAG CAG ATG CAG CTG GCG TTT GCC GCC GTT AAC GTG TGG Ala Arg Arg Lys Gln Met Gin Leu Ala Phe Ala Ala Val Asn Val Trp 845 850 855	2835
CGG AAG AAC CTG CAG GAT AGA AAG AGT GGT AGA GCA GAG CCT GAC CCT Arg Lys Asn Leu Gln Asp Arg Lys Ser Gly Arg Ala Glu Pro Asp Pro 860 865 870	2883
AAA AAG AAA GCC ACA TTT AGG GCT ATC ACC TCC ACC CTG GCT TCC AGC Lys Lys Lys Ala Thr Phe Arg Ala Ile Thr Ser Thr Leu Ala Ser Ser 875 880 885 890	2931
TTC AAG AGG CGT AGG TCC TCC AAA GAC ACG AGC ACC GGG GGT GGA CGC Phe Lys Arg Arg Ser Ser Lys Asp Thr Ser Thr Gly Gly Arg Arg 895 900 905	2979
GGT GCT TTG CAA AAC CAA AAA GAC ACA GTG CTG CCG CGA CGC GCT ATT Gly Ala Leu Gln Asn Gln Lys Asp Thr Val Leu Pro Arg Arg Ala Ile 910 915 920	3027
GAG AGG GAG GAG GGC CAG CTG CAG CTG TGT TCC CGT CAT AGG GAG AGC Glu Arg Glu Glu Gly Gln Leu Gln Leu Cys Ser Arg His Arg Glu Ser 925 930 935	3075
TGAGACTCCC CGCCCCGCCCT CCTCTGCCCG CCTCCCCCGCA GACAGACAGA CAGACGGACG	3135
GGACAGCGGC CGGGCCCCACG CAGAGCCCCG GAGCACCCACG GGGTCGGGGG AGGAGCACCC	3195
CCAGCCTCCC CGAGGCTGCC CCTGCCCGCC CGCCCGTTGG CCGGCTGGCC GGTCCACCC	3255
GTCCCCGGCCC CGCGCGTGCC CCCAGCGTGG GGCTAACGGG CGCCTTGTCT GTGTATTCT	3315
ATTTTGACAGC AGTACCATCC CACTGATATC ACGGGGCCCCG TCAACCTCTC AGATCCCTCG	3375
GTCAGCACCG TGGTGTGAGG CCCCCGGAGG CGCCCACCTG CCCAGTTAGC CGGGCCACGG	3435
ACACTGATGG GTCTCTGCTGC TCGGGAAAGG CTGAGGGAAAG CCCACCCGCC CGAGAGACTG	3495
CCCACCTGG GCCTCCCGTC CGTCTGCCCG CCCACCCGCC TGCCCTGGCGG GCAGCCCTG	3555
CTGGACCAAG GTGCGGACCG GAGCGGCTGA GGACGGGGCA GAGCTGAGTC GGCTGGCGAG	3615
GGCCCGAGGG CGCTCCGGCA GAGCCAGGCC CCTGGGGTCT CTGAGGAGTG GGGAGCCGG	3675

GCTAACTGCC CCCAGGCGGA GGGGCTTGGG GCAGAGACGG CAGCCCCATC CTTCCCGCAG	3735
CACCAGCTG AGCCACAGTG GGGCCCATGG CCCCAGCTGG CTGGGTGCC CCTCCTCGGG	3795
CGCCCTGGCT CCTCTGCAGC CTGAGCTCCA CCCTCCCCCTC TTCTTGGGGC ACCGCCACC	3855
AAACACCCCG TCTGCCCCCTT GAGGCCACAC GCCGGGGCTG GCGCTGCCCT CCCCCCACGGC	3915
CGTCCCTGAC TTCCCAGCTG GCAGCGCCTC CGCCCGCCTC GGGCCGCCTC CTCCAGAAC	3975
GAGAGGGCTG AGCCCCCTCCT CTCCTCGTCC GGCTGCAGC ACAGAAGGGG GCCTCCCCGG	4035
GGGTCCCCGG ACGCTGGCTC GGGACTGTCT TCAACCCCTGC CCTGCACCTT GGGCACGGG	4095
GAGCGCCACC CGCCCGCCCC CGCCCTCGCT CGGGGTGCGT GACCGGCCCG CCACCTTGT	4155
CAGAACCCAGC ACTCCCAGGG CCCGAGCGCG TGCCCTCCCC GTGCGCAGCC GCGCTCTGCC	4215
CCTCCGTCCC CAGGGTGCAG GCGCGCACCG CCCAACCCCC ACCTCCCGGT GTATGCAGTG	4275
GTGATGCCATA AAGGAATGTC ACG	4298

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 938 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Ser Thr Met Arg Leu Leu Thr Leu Ala Leu Leu Phe Ser Cys Ser	
1 5 10 15	
Val Ala Arg Ala Ala Cys Asp Pro Lys Ile Val Asn Ile Gly Ala Val	
20 25 30	
Leu Ser Thr Arg Lys His Glu Gln Met Phe Arg Glu Ala Val Asn Gln	
35 40 45	
Ala Asn Lys Arg His Gly Ser Trp Lys Ile Gln Leu Asn Ala Thr Ser	
50 55 60	
Val Thr His Lys Pro Asn Ala Ile Gln Met Ala Leu Ser Val Cys Glu	
65 70 75 80	
Asp Leu Ile Ser Ser Gln Val Tyr Ala Ile Leu Val Ser His Pro Pro	
85 90 95	
Thr Pro Asn Asp His Phe Thr Pro Val Ser Tyr Thr Ala Gly	
100 105 110	
Phe Tyr Arg Ile Pro Val Leu Gly Leu Thr Thr Arg Met Ser Ile Tyr	
115 120 125	
Ser Asp Lys Ser Ile His Leu Ser Phe Leu Arg Thr Val Pro Pro Tyr	
130 135 140	
Ser His Gln Ser Ser Val Trp Phe Glu Met Met Arg Val Tyr Ser Trp	
145 150 155 160	
Asn His Ile Ile Leu Leu Val Ser Asp Asp His Glu Gly Arg Ala Ala	
165 170 175	

Gln Lys Arg Leu Glu Thr Leu Leu Glu Glu Arg Glu Ser Lys Ala Glu
180 185 190

Lys Val Leu Gln Phe Asp Pro Gly Thr Lys Asn Val Thr Ala Leu Leu
195 200 205

Met Glu Ala Lys Glu Leu Glu Ala Arg Val Ile Ile Leu Ser Ala Ser
210 215 220

Glu Asp Asp Ala Ala Thr Val Tyr Arg Ala Ala Met Leu Asn Met
225 230 235 240

Thr Gly Ser Gly Tyr Val Trp Leu Val Gly Glu Arg Glu Ile Ser Gly
245 250 255

Asn Ala Leu Arg Tyr Ala Pro Asp Gly Ile Leu Gly Leu Gln Leu Ile
260 265 270

Asn Gly Lys Asn Glu Ser Ala His Ile Ser Asp Ala Val Gly Val Val
275 280 285

Ala Gln Ala Val His Glu Leu Leu Glu Lys Glu Asn Ile Thr Asp Pro
290 295 300

Pro Arg Gly Cys Val Gly Asn Thr Asn Ile Trp Lys Thr Gly Pro Leu
305 310 315 320

Phe Lys Arg Val Leu Met Ser Ser Lys Tyr Ala Asp Gly Val Thr Gly
325 330 335

Arg Val Glu Phe Asn Glu Asp Gly Asp Arg Lys Phe Ala Asn Tyr Ser
340 345 350

Ile Met Asn Leu Gln Asn Arg Lys Leu Val Gln Val Gly Ile Tyr Asn
355 360 365

Gly Thr His Val Ile Pro Asn Asp Arg Lys Ile Ile Trp Pro Gly Gly
370 375 380

Glu Thr Glu Lys Pro Arg Gly Tyr Gln Met Ser Thr Arg Leu Lys Ile
385 390 395 400

Val Thr Ile His Gln Glu Pro Phe Val Tyr Val Lys Pro Thr Leu Ser
405 410 415

Asp Gly Thr Cys Lys Glu Glu Phe Thr Val Asn Gly Asp Pro Val Lys
420 425 430

Lys Val Ile Cys Thr Gly Pro Asn Asp Thr Ser Pro Gly Ser Pro Arg
435 440 445

His Thr Val Pro Gln Cys Cys Tyr Gly Phe Cys Ile Asp Leu Leu Ile
450 455 460

Lys Leu Ala Arg Thr Met Asn Phe Thr Tyr Glu Val His Leu Val Ala
465 470 475 480

Asp Gly Lys Phe Gly Thr Gln Glu Arg Val Asn Asn Ser Asn Lys Lys
485 490 495

Glu Trp Asn Gly Met Met Gly Glu Leu Leu Ser Gly Gln Ala Asp Met
500 505 510

Ile Val Ala Pro Leu Thr Ile Asn Asn Glu Arg Ala Gln Tyr Ile Glu
515 520 525

Phe Ser Lys Pro Phe Lys Tyr Gln Gly Leu Thr Ile Leu Val Lys Lys

530	535	540
Glu Ile Pro Arg Ser Thr Leu Asp Ser Phe Met Gln Pro Phe Gln Ser		
545	550	555
560		
Thr Leu Trp Leu Leu Val Gly Leu Ser Val His Val Val Ala Val Met		
565	570	575
Leu Tyr Leu Leu Asp Arg Phe Ser Pro Phe Gly Arg Phe Lys Val Asn		
580	585	590
Ser Glu Glu Glu Glu Asp Ala Leu Thr Leu Ser Ser Ala Met Trp		
595	600	605
Phe Ser Trp Gly Val Leu Leu Asn Ser Gly Ile Gly Glu Gly Ala Pro		
610	615	620
Arg Ser Phe Ser Ala Arg Ile Leu Gly Met Val Trp Ala Gly Phe Ala		
625	630	635
640		
Met Ile Ile Val Ala Ser Tyr Thr Ala Asn Leu Ala Ala Phe Leu Val		
645	650	655
Leu Asp Arg Pro Glu Glu Arg Ile Thr Gly Ile Asn Asp Pro Arg Leu		
660	665	670
Arg Asn Pro Ser Asp Lys Phe Ile Tyr Ala Thr Val Lys Gln Ser Ser		
675	680	685
Val Asp Ile Tyr Phe Arg Arg Gln Val Glu Leu Ser Thr Met Tyr Arg		
690	695	700
His Met Glu Lys His Asn Tyr Glu Ser Ala Ala Glu Ala Ile Gln Ala		
705	710	715
720		
Val Arg Asp Asn Lys Leu His Ala Phe Ile Trp Asp Ser Ala Val Leu		
725	730	735
Glu Phe Glu Ala Ser Gln Lys Cys Asp Leu Val Thr Thr Gly Glu Leu		
740	745	750
Phe Phe Arg Ser Gly Phe Gly Ile Gly Met Arg Lys Asp Ser Pro Trp		
755	760	765
Lys Gln Asn Val Ser Leu Ser Ile Leu Lys Ser His Glu Asn Gly Phe		
770	775	780
Met Glu Asp Leu Asp Lys Thr Trp Val Arg Tyr Gln Glu Cys Asp Ser		
785	790	795
800		
Arg Ser Asn Ala Pro Ala Thr Leu Thr Phe Glu Asn Met Ala Gly Val		
805	810	815
Phe Met Leu Val Ala Gly Gly Ile Val Ala Gly Ile Phe Leu Ile Phe		
820	825	830
Ile Glu Ile Ala Tyr Lys Arg His Lys Asp Ala Arg Arg Lys Gln Met		
835	840	845
Gln Leu Ala Phe Ala Ala Val Asn Val Trp Arg Lys Asn Leu Gln Asp		
850	855	860
Arg Lys Ser Gly Arg Ala Glu Pro Asp Pro Lys Lys Lys Ala Thr Phe		
865	870	875
880		
Arg Ala Ile Thr Ser Thr Leu Ala Ser Ser Phe Lys Arg Arg Ser		

885 890 895
Ser Lys Asp Thr Ser Thr Gly Gly Gly Arg Gly Ala Leu Gln Asn Gln
900 905 910
Lys Asp Thr Val Leu Pro Arg Arg Ala Ile Glu Arg Glu Glu Gly Gln
915 920 925
Leu Gln Leu Cys Ser Arg His Arg Glu Ser
930 935

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 63 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: both
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..63

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

AGT AAA AAA AGG AAC TAT GAA AAC CTC GAC CAA CTG TCC TAT GAC AAC 48
Ser Lys Lys Arg Asn Tyr Glu Asn Leu Asp Gln Leu Ser Tyr Asp Asn
1 5 10 15
AAG CGC GGA CCC AAG 63
Lys Arg Gly Pro Lys
20

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Ser Lys Lys Arg Asn Tyr Glu Asn Leu Asp Gln Leu Ser Tyr Asp Asn
1 5 10 15
Lys Arg Gly Pro Lys
20

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4068 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: both
- (ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME KEY: CDS

(B) LOCATION: 189..3899

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

CCCTTAATAA GATTTGCTAC GTACACTCGA GCCATCGCGA GTGTTCCTTGA GCCGCGGGTG	60
ACGGTGGCTC TCGCTGCTCG CGCCCCCTCC TCCCGCGGGG GGAGCCTGAT GCCACGTTCC	120
CTATGAATTA TTTATCGCCG GCCTAAAAAT ACCCCGAACT TCACAGCCCG AGTGACCCTC	180
CGGTGGAC ATG GGT GGG GCC CTG GGG CCG GCC CTG TTG CTC ACC TCG CTC Met Gly Gly Ala Leu Gly Pro Ala Leu Leu Thr Ser Leu	230
1 5 10	
TTC GGT GCC TGG GCA GGG CTG GGT CCG GGG CAG GGC GAG CAG GGC ATG Phe Gly Ala Trp Ala Gly Leu Gly Pro Gly Gln Gly Glu Gln Gly Met	278
15 20 25 30	
ACG GTG GCC GTG GTG TTT AGC AGC TCA GGG CCG CCC CAG GCC CAG TTC Thr Val Ala Val Phe Ser Ser Gly Pro Pro Gln Ala Gln Phe	326
35 40 45	
CGT GTC CGC CTC ACC CCC CAG AGC TTC CTG GAC CTA CCC CTG GAG ATC Arg Val Arg Leu Thr Pro Gln Ser Phe Leu Asp Leu Pro Leu Glu Ile	374
50 55 60	
CAG CCG CTC ACA GTT GGG GTC AAC ACC ACC AAC CCC AGC AGC CTC CTC Gln Pro Leu Thr Val Gly Val Asn Thr Thr Asn Pro Ser Ser Leu Leu	422
65 70 75	
ACC CAG ATC TGC GGC CTC CTG GGT GCT GCC CAC GTG CAC GGC ATT GTC Thr Gln Ile Cys Gly Leu Leu Gly Ala Ala His Val His Gly Ile Val	470
80 85 90	
TTT GAG GAC AAC GTG GAC ACC GAG GCG GTG GCC CAG ATC CTT GAC TTC Phe Glu Asp Asn Val Asp Thr Glu Ala Val Ala Gln Ile Leu Asp Phe	518
95 100 105 110	
ATC TCC TCC CAG ACC CAT GTG CCC ATC CTC AGC ATC AGC GGA GGC TCT Ile Ser Ser Gln Thr His Val Pro Ile Leu Ser Ile Ser Gly Gly Ser	566
115 120 125	
GCT GTG GTG CTC ACC CCC AAG GAG CCG GGC TCC GCC TTC CTG CAG CTG Ala Val Val Leu Thr Pro Lys Glu Pro Gly Ser Ala Phe Leu Gln Leu	614
130 135 140	
GGC GTG TCC CTG GAG CAG CAG CTG CAG GTG CTG TTC AAG GTG CTG GAA Gly Val Ser Leu Glu Gln Gln Leu Gln Val Leu Phe Lys Val Leu Glu	662
145 150 155	
GAG TAC GAC TGG AGC GCC TTC GCC GTC ATC ATC AGC CTG CAC CCG GGC Glu Tyr Asp Trp Ser Ala Phe Ala Val Ile Thr Ser Leu His Pro Gly	710
160 165 170	
CAC GCG CTC TTC CTG GAG GGC GTG CGC GCC GTC GAC GGC AGC CAC His Ala Leu Phe Leu Glu Gly Val Arg Ala Val Ala Asp Ala Ser His	758
175 180 185 190	
GTG AGT TGG CGG CTG CTG GAC GTG GTC AGC CTG GAA CTG GAC CCG GGA Val Ser Trp Arg Leu Leu Asp Val Val Thr Leu Glu Leu Asp Pro Gly	806
195 200 205	
GGG CGG CGG CGG CGC ACG CAG CGC CTG CTG CGC CAG CTC GAC GCG CCC Gly Pro Arg Ala Arg Thr Gln Arg Leu Leu Arg Gln Leu Asp Ala Pro	854

210	215	220	
GTG TTT GTG GCG TAC TGC TCG CGC GAG GAG GCC GAG GTG CTC TTC GCG Val Phe Val Ala Tyr Cys Ser Arg Glu Glu Ala Glu Val Leu Phe Ala	225	230	902
GAG GCG GCG CAG GCC GGT CTG GTG GGG CCC GGC CAC GTG TGG CTG GTG Glu Ala Ala Gln Ala Gly Leu Val Gly Pro Gly His Val Trp Leu Val	240	245	950
CCC AAC CTG GCG CTG GGC AGC ACC GAT GCG CCC CCC GCC ACC TTC CCC Pro Asn Leu Ala Leu Gly Ser Thr Asp Ala Pro Pro Ala Thr Phe Pro	255	260	998
GTG GGC CTC ATC AGC GTC GTC ACC GAG AGC TGG CGC CTC AGC CTG CGC Val Gly Leu Ile Ser Val Val Thr Glu Ser Trp Arg Leu Ser Leu Arg	275	280	1046
CAG AAG GTG CGC GAC GGC GTG GCC ATT CTG GCC CTG GGC GCC CAC AGC Gln Lys Val Arg Asp Gly Val Ala Ile Leu Ala Leu Gly Ala His Ser	290	295	1094
TAC TGG CGC CAG CAT GGA ACC CTG CCA GCC CCG GCC GGG GAC TGC CGT Tyr Trp Arg Gln His Gly Thr Leu Pro Ala Pro Ala Gly Asp Cys Arg	305	310	1142
GTT CAC CCT GGG CCC GTC AGC CCT GCC CGG GAG GCC TTC TAC AGG CAC Val His Pro Gly Pro Val Ser Pro Ala Arg Glu Ala Phe Tyr Arg His	320	325	1190
CTA CTG AAT GTC ACC TGG GAG GGC CGA GAC TTC TCC TTC AGC CCT GGT Leu Leu Asn Val Thr Trp Glu Gly Arg Asp Phe Ser Phe Ser Pro Gly	335	340	1238
GGG TAC CTG GTC CAG CCC ACC ATG GTG GTG ATC GCC CTC AAC CGG CAC Gly Tyr Leu Val Gln Pro Thr Met Val Val Ile Ala Leu Asn Arg His	355	360	1286
CGC CTC TGG GAG ATG GTC GGG CGC TGG GAG CAT GGC GTC CTA TAC ATG Arg Leu Trp Glu Met Val Gly Arg Trp Glu His Gly Val Leu Tyr Met	370	375	1334
AAG TAC CCC GTG TGG CCT CGC TAC AGT GCC TCT CTG CAG CCT GTG GTG Lys Tyr Pro Val Trp Pro Arg Tyr Ser Ala Ser Leu Gln Pro Val Val	385	390	1382
GAC AGT CGG CAC CTG ACG GTG GCC ACG CTG GAA GAG CGG CCC TTT GTC Asp Ser Arg His Leu Thr Val Ala Thr Leu Glu Arg Pro Phe Val	400	405	1430
ATC GTG GAG AGC CCT GAC CCT GGC ACA GGA GGC TGT GTC CCC AAC ACC Ile Val Glu Ser Pro Asp Pro Gly Thr Gly Gly Cys Val Pro Asn Thr	415	420	1478
GTG CCC TGC CGC AGG CAG AGC AAC CAC ACC TTC AGC AGC GGG GAC GTG Val Pro Cys Arg Arg Gln Ser Asn His Thr Phe Ser Ser Gly Asp Val	435	440	1526
GCC CCC TAC ACC AAG CTC TGC TGT AAG GGA TTC TGC ATC GAC ATC CTC Ala Pro Tyr Thr Lys Leu Cys Cys Lys Gly Phe Cys Ile Asp Ile Leu	450	455	1574
AAG AAG CTG GCG AGA GTG GTC AAA TTC TCC TAC GAC CTG TAC CTG GTG Lys Lys Leu Ala Arg Val Val Lys Phe Ser Tyr Asp Leu Tyr Leu Val	465	470	1622
ACC AAC GGC AAG CAT GGC AAG CGG GTG CGC GGC GTA TGS AAC GGC ATG			1670

Thr Asn Glu Lys His Gly Lys Arg Val Arg Gly Val Trp Asn Gly Met
485 490

ATT GGG GAG GTC TAC TAC AAG CGG GCA GAC ATG GCC ATC GGC TCC CTC 1718
Ile Gly Glu Val Tyr Tyr Lys Arg Ala Asp Met Ala Ile Gly Ser Leu
495 500 505 510

ACC ATC AAT GAG GAA CGC TCC GAG ATC GTA GAC TTC TCT GTA CCC TTT 1766
Thr Ile Asn Glu Glu Arg Ser Glu Ile Val Asp Phe Ser Val Pro Phe
515 520 525

GTG GAG ACG GGC ATC AGT GTG ATG GTG GCT CGC AGC AAT GGC ACC GTC 1814
Val Glu Thr Gly Ile Ser Val Met Val Ala Arg Ser Asn Gly Thr Val
530 535 540

TCC CCC TCG GGC TTC TTG GAG CCA TAT AGC CCT GCA GTG TGG GTG ATG 1862
Ser Pro Ser Ala Phe Leu Glu Pro Tyr Ser Pro Ala Val Trp Val Met
545 550 555

ATG TTT GTC ATG TGC CTC ACT GTG GTG GCC ATC ACC GTC TTC ATG TTC 1910
Met Phe Val Met Cys Leu Thr Val Val Ala Ile Thr Val Phe Met Phe
560 565 570

GAG TAC TTC AGC CCT GTC AGC TAC AAC CAG AAC CTC ACC AGA GGC AAG 1958
Glu Tyr Phe Ser Pro Val Ser Tyr Asn Gln Asn Leu Thr Arg Gly Lys
575 580 585 590

AAG TCC GGG GGC CCA GCT TTC ACT ATC GGC AAG TCC GTG TGG CTG CTG 2006
Lys Ser Gly Glu Pro Ala Phe Thr Ile Gly Lys Ser Val Trp Leu Leu
595 600 605

TGG GCG CTG GTC TTC AAC AAC TCA GTG CCC ATC GAG AAC CGG CGG GGC 2054
Trp Ala Leu Val Phe Asn Asn Ser Val Pro Ile Glu Asn Pro Arg Gly
610 615 620

ACC ACC AGC AAG ATC ATG GTT CTG GTC TGG GCC TTC TTT GCT GTC ATC 2102
Thr Thr Ser Lys Ile Met Val Leu Val Trp Ala Phe Phe Ala Val Ile
625 630 635

TTC CTC GCC AGA TAC ACG GGC AAC CTG GCC GCC TTC ATG ATC CAA GAG 2150
Phe Leu Ala Arg Tyr Thr Ala Asn Leu Ala Ala Phe Met Ile Gln Glu
640 645 650

CAA TAC ATC GAC ACT GTG TCG GGC CTC AGT GAC AAG AAG TTT CAG CGG 2198
Gln Tyr Ile Asp Thr Val Ser Gly Leu Ser Asp Lys Lys Phe Gln Arg
655 660 665 670

CCT CAA GAT CAG TAC CCA CCT TTC CGC TTC GGC ACG GTG CCC AAC GGC 2246
Pro Gln Asp Gln Tyr Pro Pro Phe Arg Phe Gly Thr Val Pro Asn Gly
675 680 685

AGC ACG GAG CGG AAC ATC CGC AGT AAC TAC CGT GAC ATG CAC ACC CAC 2294
Ser Thr Glu Arg Asn Ile Arg Ser Asn Tyr Arg Asp Met His Thr His
690 695 700

ATG GTC AAC TTC AAC CGG CGC TCG GTG GAG GAC GCG CTC ACC AGC CTC 2342
Met Val Lys Phe Asn Gln Arg Ser Val Glu Asp Ala Leu Thr Ser Leu
705 710 715

AAG ATG GGG AAG CTG GAT GCC TTC ATC TAT GAT GCT GCT GTC CTC AAC 2390
Lys Met Gly Lys Leu Asp Ala Phe Ile Tyr Asp Ala Ala Val Leu Asn
720 725 730

TAC ATG GCA GGC AAG GAC GAG GGC TGC AAG CTG GTC ACC ATT GGG TCT 2438
Tyr Met Ala Gly Lys Asp Glu Gly Cys Lys Leu Val Thr Ile Gly Ser
735 740 745 750

GGC AAG GTC TTT GCT ACC ACT GGC TAC GGC ATG GCC ATG CAG AAG GAC Gly Lys Val Phe Ala Thr Thr Gly Tyr Gly Ile Ala Met Gln Lys Asp 755 760 765	2436
TCC CAC TGG AAG CGG GCG ATA GAC CTG GCG CTC TTG CAG TTC CTG GGG Ser His Trp Lys Arg Ala Ile Asp Leu Ala Leu Gln Phe Leu Gly 770 775 780	2534
GAC GGA GAG ACA CAG AAA CTG GAG ACA GTG TGG CTC TCA GGG ATC TGC Asp Gly Glu Thr Gln Lys Leu Glu Thr Val Trp Leu Ser Gly Ile Cys 785 790 795	2582
CAG AAT GAG AAG AAC GAG GTG ATG AGC AGC AAG CTG GAC ATC GAC AAC Gln Asn Glu Lys Asn Glu Val Met Ser Ser Lys Leu Asp Ile Asp Asn 800 805 810	2630
ATG GGA GGC GTC TTC TAC ATG CTG CTG GTG GCC ATG GGG CTG GCC CTG Met Gly Val Phe Tyr Met Leu Leu Val Ala Met Gly Leu Ala Leu 815 820 825 830	2678
CTG GTC TTC GCC TGG GAG CAC CTG GTC TAC TGG AAG CTG CGC CAC TCG Leu Val Phe Ala Trp Glu His Leu Val Tyr Trp Lys Leu Arg His Ser 835 840 845	2726
GTG CCC AAC TCA TCC CAG CTG GAC TTT CTG CTG GCT TTC AGC AGG GGC Val Pro Asn Ser Ser Gln Leu Asp Phe Leu Leu Ala Phe Ser Arg GLY 850 855 860	2774
ATC TAC AGC TGC TTC AGC GGG GTG CAG AGC CTC GCC AGC CCA CCG CGG Ile Tyr Ser Cys Phe Ser Gly Val Gln Ser Leu Ala Ser Pro Pro Arg 865 870 875	2822
CAG GCC AGC CCG GAC CTC ACG GCG AGC TCG GCC CAG GCC AGC GTG CTC Gln Ala Ser Pro Asp Leu Thr Ala Ser Ser Ala Gln Ala Ser Val Leu 880 885 890	2870
AAG ATT CTG CAG GCA GCG CGC GAC ATG GTG ACC ACG GCG GGC GTA AGC Lys Ile Leu Gln Ala Ala Arg Asp Met Val Thr Thr Ala Gly Val Ser 895 900 905 910	2918
AAC TCC CTG GAC CGC GCG ACT CGC ACC ATC GAG AAT TGG GGT GGC GGC Asn Ser Leu Asp Arg Ala Thr Arg Thr Ile Glu Asn Trp Gly Gly GLY 915 920 925	2966
CGC CGT CGC CCC CCA CGG TCC CCC TGC CCG ACC CCG CGG TCT GGC CCC Arg Arg Ala Pro Pro Pro Ser Pro Cys Pro Thr Pro Arg Ser Gly Pro 930 935 940	3014
AGC CCA TGC CTG CCC ACC CGG GAC CGG CCC CCA GAG CCG AGC CCC ACG Ser Pro Cys Leu Pro Thr Pro Asp Pro Pro Pro Glu Pro Ser Pro Thr 945 950 955	3062
GGC TGG GGA CCG CCA GAC GGG GGT CGC GCG GCG CTT GTG CGC AGG GCT Gly Trp Gly Pro Pro Asp Gly Gly Arg Ala Ala Leu Val Arg Arg Ala 960 965 970	3110
CCG CAG CCC CCG GGC CGC CGG CCG ACG CCG GGG CCG CCC CTG TCC GAC Pro Gln Pro Pro Gly Arg Pro Pro Thr Pro Gly Pro Pro Leu Ser Asp 975 980 985 990	3158
GTC TCC CGA GTG TCG CGC CGC CCA CGG TGG GAG GCG CGG TGG CGG GTG Val Ser Arg Val Ser Arg Arg Pro Ala Trp Glu Ala Arg Trp Pro Val 995 1000 1005	3206
CGG ACC GGG CAC TGC GGG AGG CAC CTC TCG GCC TCC GAG CGG CGG CCC CTG Arg Thr Gly His Cys Gly Arg His Leu Ser Ala Ser Glu Arg Pro Leu 1010 1015 1020	3254

TCG CCC GCG CGC TGT CAC TAC AGC TCC TTT CCT CGA GCC GAC CGA TCC Ser Pro Ala Arg Cys His Tyr Ser Ser Phe Pro Arg Ala Asp Arg Ser 1025 1030 1035	3302
GCG CCC CCC TTC CTC CCG CTC TTC CCG GAG CCC CCG GAG CTG GAG GAC Gly Arg Pro Phe Leu Pro Leu Phe Pro Glu Pro Pro Glu Leu Glu Asp 1040 1045 1050	3350
CTG CCG CTG CTC GGT CCG GAG CAG CTG GCC CGG CGG GAG GCC CTG CTG Leu Pro Leu Leu Gly Pro Glu Gln Leu Ala Arg Arg Glu Ala Leu Leu 1055 1060 1065 1070	3398
AAC GCG GCC TGG GCC CGG GGC TCG CGC CCG AGT CAC GCT TCC CTG CCC Asn Ala Ala Trp Ala Arg Gly Ser Arg Pro Ser His Ala Ser Leu Pro 1075 1080 1085	3446
AGC TCC GTG GCC GAG GCC TTC GCT CGG CCC AGC TCG CTG CCC GCT GGG Ser Ser Val Ala Glu Ala Phe Ala Arg Pro Ser Ser Leu Pro Ala Gly 1090 1095 1100	3494
TGC ACC GGC CCC GCC TGC GCC CGC CCC GAC GGC CAC TCG GCC TGC AGG Cys Thr Gly Pro Ala Cys Ala Arg Pro Asp Gly His Ser Ala Cys Arg 1105 1110 1115	3542
CGC TTG GCG CAG GCG CAG TCG ATG TGC TTG CGG ATC TAC CGG GAG GCC Arg Leu Ala Gln Ala Gln Ser Met Cys Leu Pro Ile Tyr Arg Glu Ala 1120 1125 1130	3590
TGC CAG GAG GGC GAG CAG GCA GGG GCC CCC GCG TGG CAG CAC AGA CAG Cys Gln Glu Gly Glu Gln Ala Gly Ala Pro Ala Trp Gln His Arg Gln 1135 1140 1145 1150	3638
CAC GTC TGC CTG CAC GCC CAC CTC CCA TTG TGC TGG GGG GCT His Val Cys Leu His Ala His Leu Pro Leu Cys Trp Gly Ala 1155 1160 1165	3686
GTC TGT CCT CAC CTT CCA CCC TGT GAC AGC CAC GGC TCC TGG CTC TCC Val Cys Pro His Leu Pro Pro Cys Asp Ser His Gly Ser Trp Leu Ser 1170 1175 1180	3734
GCG GCC TGG GGG CCT CTG GGG CAC AGC GGC AGG ACT CTG GGG CTG GGC Gly Ala Trp Gly Pro Leu Gly His Ser Gly Arg Thr Leu Gly Leu Gly 1185 1190 1195	3782
ACA GGC TAC AGA GAC AGT GGG GGA CTG GAC GAG ATC AGC AGT GTA GCC Thr Gly Tyr Arg Asp Ser Gly Gly Leu Asp Glu Ile Ser Ser Val Ala 1200 1205 1210	3830
CGT GGG ACG CAA GGC TTC CCG GGA CCC TGC ACC TGG AGA CGG ATC TCC Arg Gly Thr Gln Gly Phe Pro Gly Pro Cys Thr Trp Arg Arg Ile Ser 1215 1220 1225 1230	3873
AGT CTG GAG TCA GAA GTG TGAGTTATCA GCCACTCAGG CTCCGAGCCA Ser Leu Glu Ser Glu Val 1235	3926
GCTGGATTCT CTGCCTGCCA CTGTCAGGGT TAAGCGGCAG GCAGGGTTGG CCCTTCTCTG	3986
GCTTCTACCA TGAAATCCTG GCCATGGCAC CCCAGTGACA GATGATGTCT TCCATGGTCA	4046
TCACTGACCT CAGCTAGCCT CA	4068

.2. INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1236 amino acids

(B) TYPE: amino acid
(C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Gly Gly Ala Leu Gly Pro Ala Leu Leu Leu Thr Ser Leu Phe Gly
1 5 10 15

Ala Trp Ala Gly Leu Gly Pro Gly Gln Gly Glu Gln Gly Met Thr Val
20 25 30

Ala Val Val Phe Ser Ser Ser Gly Pro Pro Gln Ala Gln Phe Arg Val
35 40 45

Arg Leu Thr Pro Gln Ser Phe Leu Asp Leu Pro Leu Glu Ile Gln Pro
50 55 60

Leu Thr Val Gly Val Asn Thr Thr Asn Pro Ser Ser Leu Leu Thr Gln
65 70 75 80

Ile Cys Gly Leu Leu Gly Ala Ala His Val His Gly Ile Val Phe Glu
85 90 95

Asp Asn Val Asp Thr Glu Ala Val Ala Gln Ile Leu Asp Phe Ile Ser
100 105 110

Ser Gln Thr His Val Pro Ile Leu Ser Ile Ser Gly Gly Ser Ala Val
115 120 125

Val Leu Thr Pro Lys Glu Pro Gly Ser Ala Phe Leu Gln Leu Gly Val
130 135 140

Ser Leu Glu Gln Gln Leu Gln Val Leu Phe Lys Val Leu Glu Glu Tyr
145 150 155 160

Asp Trp Ser Ala Phe Ala Val Ile Thr Ser Leu His Pro Gly His Ala
165 170 175

Leu Phe Leu Glu Gly Val Arg Ala Val Ala Asp Ala Ser His Val Ser
180 185 190

Trp Arg Leu Leu Asp Val Val Thr Leu Glu Leu Asp Pro Gly Gly Pro
195 200 205

Arg Ala Arg Thr Gln Arg Leu Leu Arg Gln Leu Asp Ala Pro Val Phe
210 215 220

Val Ala Tyr Cys Ser Arg Glu Glu Ala Glu Val Leu Phe Ala Glu Ala
225 230 235 240

Ala Gln Ala Gly Leu Val Gly Pro Gly His Val Trp Leu Val Pro Asn
245 250 255

Leu Ala Leu Gly Ser Thr Asp Ala Pro Pro Ala Thr Phe Pro Val Gly
260 265 270

Leu Ile Ser Val Val Thr Glu Ser Trp Arg Leu Ser Leu Arg Gln Lys
275 280 285

Val Arg Asp Gly Val Ala Ile Leu Ala Leu Gly Ala His Ser Tyr Trp
290 295 300

Arg Gln His Gly Thr Leu Pro Ala Pro Ala Gly Asp Cys Arg Val His
305 310 315 320

Pro Gly Pro Val Ser Pro Ala Arg Glu Ala Phe Tyr Arg His Leu Leu
325 330 335

Asn Val Thr Trp Glu Gly Arg Asp Phe Ser Phe Ser Pro Gly Gly Tyr
340 345 350

Leu Val Gln Pro Thr Met Val Val Ile Ala Leu Asn Arg His Arg Leu
355 360 365

Trp Glu Met Val Gly Arg Trp Glu His Gly Val Leu Tyr Met Lys Tyr
370 375 380

Pro Val Trp Pro Arg Tyr Ser Ala Ser Leu Gln Pro Val Val Asp Ser
385 390 395 400

Arg His Leu Thr Val Ala Thr Leu Glu Glu Arg Pro Phe Val Ile Val
405 410 415

Glu Ser Pro Asp Pro Gly Thr Gly Gly Cys Val Pro Asn Thr Val Pro
420 425 430

Cys Arg Arg Gln Ser Asn His Thr Phe Ser Ser Gly Asp Val Ala Pro
435 440 445

Tyr Thr Lys Leu Cys Cys Lys Gly Phe Cys Ile Asp Ile Leu Lys Lys
450 455 460

Leu Ala Arg Val Val Lys Phe Ser Tyr Asp Leu Tyr Leu Val Thr Asn
465 470 475 480

Gly Lys His Gly Lys Arg Val Arg Gly Val Trp Asn Gly Met Ile Gly
485 490 495

Glu Val Tyr Tyr Lys Arg Ala Asp Met Ala Ile Gly Ser Leu Thr Ile
500 505 510

Asn Glu Glu Arg Ser Glu Ile Val Asp Phe Ser Val Pro Phe Val Glu
515 520 525

Thr Gly Ile Ser Val Met Val Ala Arg Ser Asn Gly Thr Val Ser Pro
530 535 540

Ser Ala Phe Leu Glu Pro Tyr Ser Pro Ala Val Trp Val Met Met Phe
545 550 555 560

Val Met Cys Leu Thr Val Val Ala Ile Thr Val Phe Met Phe Glu Tyr
565 570 575

Phe Ser Pro Val Ser Tyr Asn Gln Asn Leu Thr Arg Gly Lys Lys Ser
580 585 590

Gly Gly Pro Ala Phe Thr Ile Gly Lys Ser Val Trp Leu Leu Trp Ala
595 600 605

Leu Val Phe Asn Asn Ser Val Pro Ile Glu Asn Pro Arg Gly Thr Thr
610 615 620

Ser Lys Ile Met Val Leu Val Trp Ala Phe Phe Ala Val Ile Phe Leu
625 630 635 640

Ala Arg Tyr Thr Ala Asn Leu Ala Ala Phe Met Ile Gln Glu Gln Tyr
645 650 655

Ile Asp Thr Val Ser Gly Leu Ser Asp Lys Lys Phe Gln Arg Pro Gln
660 665 670

Asp Gln Tyr Pro Pro Phe Arg Phe Gly Thr Val Pro Asn Gly Ser Thr
675 680 685

Glu Arg Asn Ile Arg Ser Asn Tyr Arg Asp Met His Thr His Met Val
690 695 700

Lys Phe Asn Gln Arg Ser Val Glu Asp Ala Leu Thr Ser Leu Lys Met
705 710 715 720

Gly Lys Leu Asp Ala Phe Ile Tyr Asp Ala Ala Val Leu Asn Tyr Met
725 730 735

Ala Gly Lys Asp Glu Gly Cys Lys Leu Val Thr Ile Gly Ser Gly Lys
740 745 750

Val Phe Ala Thr Thr Gly Tyr Gly Ile Ala Met Gln Lys Asp Ser His
755 760 765

Trp Lys Arg Ala Ile Asp Leu Ala Leu Leu Gln Phe Leu Gly Asp Gly
770 775 780

Glu Thr Gln Lys Leu Glu Thr Val Trp Leu Ser Gly Ile Cys Gln Asn
785 790 795 800

Glu Lys Asn Glu Val Met Ser Ser Lys Leu Asp Ile Asp Asn Met Gly
805 810 815

Gly Val Phe Tyr Met Leu Leu Val Ala Met Gly Leu Ala Leu Leu Val
820 825 830

Phe Ala Trp Glu His Leu Val Tyr Trp Lys Leu Arg His Ser Val Pro
835 840 845

Asn Ser Ser Gln Leu Asp Phe Leu Leu Ala Phe Ser Arg Gly Ile Tyr
850 855 860

Ser Cys Phe Ser Gly Val Gln Ser Leu Ala Ser Pro Pro Arg Gln Ala
865 870 875 880

Ser Pro Asp Leu Thr Ala Ser Ser Ala Gln Ala Ser Val Leu Lys Ile
885 890 895

Leu Gln Ala Ala Arg Asp Met Val Thr Thr Ala Gly Val Ser Asn Ser
900 905 910

Leu Asp Arg Ala Thr Arg Thr Ile Glu Asn Trp Gly Gly Arg Arg
915 920 925

Ala Pro Pro Pro Ser Pro Cys Pro Thr Pro Arg Ser Gly Pro Ser Pro
930 935 940

Cys Leu Pro Thr Pro Asp Pro Pro Pro Glu Pro Ser Pro Thr Gly Trp
945 950 955 960

Gly Pro Pro Asp Gly Gly Arg Ala Ala Leu Val Arg Arg Ala Pro Gln
965 970 975

Pro Pro Gly Arg Pro Pro Thr Pro Gly Pro Pro Leu Ser Asp Val Ser
980 985 990

Arg Val Ser Arg Arg Pro Ala Trp Glu Ala Arg Trp Pro Val Arg Thr
995 1000 1005

Gly His Cys Gly Arg His Leu Ser Ala Ser Glu Arg Pro Leu Ser Pro
1010 1015 1020

Ala Arg Cys His Tyr Ser Ser Phe Pro Arg Ala Asp Arg Ser Gly Arg
1025 1030 1035 1040

Pro Phe Leu Pro Leu Phe Pro Glu Pro Pro Glu Leu Glu Asp Leu Pro
1045 1050 1055

Leu Leu Gly Pro Glu Gln Leu Ala Arg Arg Glu Ala Leu Leu Asn Ala
1060 1065 1070

Ala Trp Ala Arg Gly Ser Arg Pro Ser His Ala Ser Leu Pro Ser Ser
1075 1080 1085

Val Ala Glu Ala Phe Ala Arg Pro Ser Ser Leu Pro Ala Gly Cys Thr
1090 1095 1100

Gly Pro Ala Cys Ala Arg Pro Asp Gly His Ser Ala Cys Arg Arg Leu
1105 1110 1115 1120

Ala Gln Ala Gln Ser Met Cys Leu Pro Ile Tyr Arg Glu Ala Cys Gln
1125 1130 1135

Glu Gly Glu Gln Ala Gly Ala Pro Ala Trp Gln His Arg Gln His Val
1140 1145 1150

Cys Leu His Ala His Leu Pro Leu Cys Trp Gly Ala Val Cys
1155 1160 1165

Pro His Leu Pro Pro Cys Asp Ser His Gly Ser Trp Leu Ser Gly Ala
1170 1175 1180

Trp Gly Pro Leu Gly His Ser Gly Arg Thr Leu Gly Leu Gly Thr Gly
1185 1190 1195 1200

Tyr Arg Asp Ser Gly Gly Leu Asp Glu Ile Ser Ser Val Ala Arg Gly
1205 1210 1215

Thr Gln Gly Phe Pro Gly Pro Cys Thr Trp Arg Arg Ile Ser Ser Leu
1220 1225 1230

Glu Ser Glu Val
1235

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME, KEY: CDS
(B) LOCATION: 2..22

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

C TCT GAG GCT CAG CCT GTC CCC AG
Ser Glu Ala Gln Pro Val Pro
1 5

(1) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Ser Glu Ala Gln Pro Val Pro
1 5

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

AGAAGGGGGT G 11

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4808 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 311..4705

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

ATCATGGGAC CGGGTGAGCG CTGAGAACG CGGCCGCAGC CATCACCCCT GGAGATGACC	60
AGGAGCGGCC ATGTGCTGAGA ACTATGTGGA GAGAGGCTGC GAGCCCTGCT GCAGAGCCTC	120
CGGCTGGGAT AGCCGCCCCC CGTGGGGCG ATGCGGACAG CGGGGACAG CCAGGGGAGC	180
GCGCTGGGCG CGTAGCATGC GGGAAACCGC TAAACCCGGT GGCTGCTGAG GCGGGCGAGA	240
TGCTCGTGCG CGCAAGCGCGC CCCACTGCAT CCTCGACCTT CTCGGGCTAC AGGGACCGTC	300
AGTGGCGACT ATG GGC AGA GTG GGC TAT TGG ACC CTG CTG GTG CTG CCG Met Gly Arg Val Gly Tyr Trp Thr Leu Leu Val Leu Pro	349
1 5 10	
GCG CTG CTG GTC TGG CGC GGT CCG GCG CCG AGC GCG GCG GCG GAG AAG Ala Leu Leu Val Trp Arg Gly Pro Ala Pro Ser Ala Ala Glu Lys	397
15 20 25	
GGT CCC CCC GCG CTA AAT ATT GCG GTG ATG CTG GGT CAC AGC CAC GAC	445

Gly Pro Pro Ala Leu Asn Ile Ala Val Met Leu Gly His Ser His Asp			
30	35	40	45
GTG ACA GAG CGC GAA CTT CGA ACA CTG TGG GGC CCC GAG CAG GCG GCG			493
Val Thr Glu Arg Glu Leu Arg Thr Leu Trp Gly Pro Glu Gln Ala Ala			
50	55	60	
GGG CTG CCC CTG GAC GTG AAC GTG GTA GCT CTG ATG AAC CGC ACC			541
Gly Leu Pro Leu Asp Val Asn Val Val Ala Leu Leu Met Asn Arg Thr			
65	70	75	
GAC CCC AAG AGC CTC ATC ACG CAC GTG TGC GAC CTC ATG TCC GGG GCA			589
Asp Pro Lys Ser Leu Ile Thr His Val Cys Asp Leu Met Ser Gly Ala			
80	85	90	
CGC ATC CAC GGC CTC GTG TTT GGG GAC GAC ACG GAC CAG GAG GCC GTA			637
Arg Ile His Gly Leu Val Phe Gly Asp Asp Thr Asp Gln Glu Ala Val			
95	100	105	
GCC CAG ATG CTG GAT TTT ATC TCC TCC CAC ACC TTC GTC CCC ATC TTG			685
Ala Gln Met Leu Asp Phe Ile Ser Ser His Thr Phe Val Pro Ile Leu			
110	115	120	125
GGC ATT CAT GGG GGC GCA TCT ATG ATC ATG GCT GAC AAG GAT CCG ACG			733
Gly Ile His Gly Gly Ala Ser Met Ile Met Ala Asp Lys Asp Pro Thr			
130	135	140	
TCT ACC TTC TTC CAG TTT GGA GCG TCC ATC CAG CAG CAA GCC ACG GTC			781
Ser Thr Phe Gln Phe Gly Ala Ser Ile Gln Gln Gln Ala Thr Val			
145	150	155	
ATG CTG AAG ATC ATG CAG GAT TAT GAC TGG CAT GTC TTC TCC CTG GTG			829
Met Leu Lys Ile Met Gln Asp Tyr Asp Trp His Val Phe Ser Leu Val			
160	165	170	
ACC ACT ATC TTC CCT GGC TAC AGG GAA TTC ATC AGC TTC GTC AAG ACC			877
Thr Thr Ile Phe Pro Gly Tyr Arg Glu Phe Ile Ser Phe Val Lys Thr			
175	180	185	
ACA GTG GAC AAC AGC TTT GTG GGC TGG GAC ATG CAG AAT GTG ATC ACA			925
Thr Val Asp Asn Ser Phe Val Gly Trp Asp Met Gln Asn Val Ile Thr			
190	195	200	205
CTG GAC ACT TCC TTT GAG GAT GCA AAG ACA CAA GTC CAG CTG AAG AAG			973
Leu Asp Thr Ser Phe Glu Asp Ala Lys Thr Gln Val Gln Leu Lys Lys			
210	215	220	
ATC CAC TCT TCT GTC ATC TTG CTC TAC TGT TCC AAA GAC GAG GCT GTT			1021
Ile His Ser Ser Val Ile Leu Leu Tyr Cys Ser Lys Asp Glu Ala Val			
225	230	235	
CTC ATT CTG AGT GAG GCC CGC TCC CTT GGC CTC ACC GGG TAT GAT TTC			1069
Leu Ile Leu Ser Glu Ala Arg Ser Leu Gly Leu Thr Gly Tyr Asp Phe			
240	245	250	
TTC TGG ATT GTC CGC AGC TTG GTC TCT GGG AAC ACG GAG CTC ATC CCA			1117
Phe Trp Ile Val Pro Ser Leu Val Ser Gly Asn Thr Glu Leu Ile Pro			
255	260	265	
AAA GAG TTT CCA TCG GGA CTC ATT TCT GTC TCC TAC GAT GAC TGG GAC			1165
Lys Glu Phe Pro Ser Gly Leu Ile Ser Val Ser Tyr Asp Asp Trp Asp			
270	275	280	285
TAC AGC CTG GAG GCG AGA GTG AGG GAC GGC ATT GGC ATC CTA ACC ACC			1213
Tyr Ser Leu Glu Ala Arg Val Arg Asp Gly Ile Gly Ile Leu Thr Thr			
290	295	300	

GCT GCA TCT TCT ATG CTC GAG AAG TTC TCC TAC ATC CCC GAG GCC AAG Ala Ala Ser Ser Met Leu Glu Lys Phe Ser Tyr Ile Pro Glu Ala Lys 305 310 315	1261
GCC AGC TGC TAC GGG CAG ATG GAG AGG CCA GAG GTC CCG ATG CAC ACC Ala Ser Cys Tyr Gly Gln Met Glu Arg Pro Glu Val Pro Met His Thr 320 325 330	1309
TTG CAC CCA TTT ATG GTC AAT GTT ACA TGG GAT GGC AAA GAC TTA TCC Leu His Pro Phe Met Val Asn Val Thr Trp Asp Gly Lys Asp Leu Ser 335 340 345	1357
TTC ACT GAG GAA GGC TAC CAG GTG CAC CCC AGG CTG GTG GTG ATT GTG Phe Thr Glu Glu Gly Tyr Gln Val His Pro Arg Leu Val Val Ile Val 350 355 360 365	1405
CTG AAC AAA GAC CGG GAA TGG GAA AAG GTG GGC AAG TGG GAG AAC CAT Leu Asn Lys Asp Arg Glu Trp Glu Lys Val Gly Lys Trp Glu Asn His 370 375 380	1453
ACG CTG AGC CTG AGG CAC GCC GTG TGG CCC AGG TAC AAG TCC TTC TCC Thr Leu Ser Leu Arg His Ala Val Trp Pro Arg Tyr Lys Ser Phe Ser 385 390 395	1501
GAC TGT GAG CCG GAT GAC AAC CAT CTC AGC ATC GTC ACC CTG GAG GAS Asp Cys Glu Pro Asp Asp Asn His Leu Ser Ile Val Thr Leu Glu Glu 400 405 410	1549
GCC CCA TTG GTC ATC GTG GAA GAC ATA GAC CCC CTG ACC GAG ACG TGT Ala Pro Phe Val Ile Val Glu Asp Ile Asp Pro Leu Thr Glu Thr Cys 415 420 425	1597
GTG AGG AAC ACC GTG CCA TGT CGG AAG TTC GTC AAA ATC AAC AAT TCA Val Arg Asn Thr Val Pro Cys Arg Lys Phe Val Lys Ile Asn Asn Ser 430 435 440 445	1645
ACC AAT GAG GGG ATG AAT GTG AAG AAA TGC TGC AAG GGG TTC TGC ATT Thr Asn Glu Gly Met Asn Val Lys Lys Cys Cys Lys Gly Phe Cys Ile 450 455 460	1693
GAT ATT CTG AAG AAG CTT TCC AGA ACT GTG AAG TTT ACT TAC GAC CTC Asp Ile Leu Lys Leu Ser Arg Thr Val Lys Phe Thr Tyr Asp Leu 465 470 475	1741
TAT CTG GTG ACC AAT GGG AAG CAT GGC AAG AAA GTT AAC AAT GTG TGG Tyr Leu Val Thr Asn Gly Lys His Gly Lys Lys Val Asn Asn Val Trp 480 485 490	1789
AAT GGA ATG ATC GGT GAA GTG GTC TAT CAA CGG GCA GTC ATG GCA GTT Asn Gly Met Ile Gly Glu Val Val Tyr Gln Arg Ala Val Met Ala Val 495 500 505	1837
GGC TCG CTC ACC ATC AAT GAG GAA CGT TCT GAA GTG GTG GAC TTC TCT Gly Ser Leu Thr Ile Asn Glu Glu Arg Ser Glu Val Val Asp Phe Ser 510 515 520 525	1885
GTG CCC TTT GTG GAA ACG GGA ATC AGT GTC ATG GTT TCA AGA AGT AAT Val Pro Phe Val Glu Thr Gly Ile Ser Val Met Val Ser Arg Ser Asn 530 535 540	1933
GGC ACC GTC TCA CCT TCT GCT TTT CTA GAA CCA TTC AGC GCC TCT GTC Gly Thr Val Ser Pro Ser Ala Phe Leu Glu Pro Phe Ser Ala Ser Val 545 550 555	1981
TGG GTG ATG ATG TTT GTG ATG CTG CTC ATT GTT TCT GCC ATA GCT GTT Trp Val Met Met Phe Val Met Leu Leu Ile Val Ser Ala Ile Ala Val 560 565 570	2029

TGG	GTC	TTG	GAT	TAC	TCC	AGC	CCT	GTT	GGA	TAC	AAC	AGA	AAC	TTA	GCC	2077
Trp	Val	Leu	Asp	Tyr	Ser	Ser	Pro	Val	Gly	Tyr	Asn	Arg	Asn	Leu	Ala	
575					580				585							
AAA	GGG	AAA	GCA	CCC	CAT	GGG	CCT	TCT	TTT	ACA	ATT	GGA	AAA	GCT	ATA	2125
Lys	Gly	Lys	Ala	Pro	His	Gly	Pro	Ser	Phe	Thr	Ile	Gly	Lys	Ala	Ile	
590					595				600						605	
TGG	CTT	CTT	TGG	GGC	CTG	GTG	TTC	ATC	AAC	TCC	GTG	CCT	GTC	CAG	AAT	2173
Trp	Leu	Leu	Trp	Gly	Leu	Val	Phe	Asn	Asn	Ser	Val	Pro	Val	Gln	Asn	
							610		615					620		
CCT	AAA	GGG	ACC	ACC	AGC	AAG	ATC	ATG	GTA	TCT	GTA	TGG	GCC	TTC	TTC	2221
Pro	Lys	Gly	Thr	Thr	Ser	Lys	Ile	Met	Val	Ser	Val	Trp	Ala	Phe	Phe	
							625		630				635			
GCT	GTC	ATA	TTC	CTG	GCT	AGC	TAC	ACA	GCC	AAT	CTG	GCT	GCC	TTC	ATG	2269
Ala	Val	Ile	Phe	Leu	Ala	Ser	Tyr	Thr	Ala	Asn	Leu	Ala	Ala	Phe	Met	
							640		645				650			
ATC	CAA	GAG	GAA	TTT	GTG	GAC	CAA	GTG	ACC	GGC	CTC	AGT	GAC	AAA	AAG	2317
Ile	Gln	Glu	Glu	Phe	Val	Asp	Gln	Val	Thr	Gly	Leu	Ser	Asp	Lys	Lys	
							655		660				665			
TTT	CAG	AGA	CCT	CAT	GAC	TAT	TCC	CCA	CCT	TTT	CGA	TTT	GGG	ACA	GTG	2365
Phe	Gln	Arg	Pro	His	Asp	Tyr	Ser	Pro	Pro	Phe	Arg	Phe	Gly	Thr	Val	
							670		675				680		685	
CCT	AAT	GGA	AGC	ACG	GAG	AGA	AAC	ATT	CGG	AAT	AAC	TAT	CCC	TAC	ATG	2413
Pro	Asn	Gly	Ser	Thr	Glu	Arg	Asn	Ile	Arg	Asn	Asn	Tyr	Pro	Tyr	Met	
							690		695				700			
CAT	CAG	TAC	ATG	ACC	AAA	TTT	AAT	CAG	AAA	GGA	GTA	GAG	GAC	GCC	TTG	2461
His	Gln	Tyr	Met	Thr	Lys	Phe	Asn	Gln	Lys	Gly	Val	Glu	Asp	Ala	Leu	
							705		710				715			
GTC	AGC	CTG	AAA	ACG	GGG	AAG	CTG	GAC	GCT	TTC	ATC	TAC	GAT	GCC	GCA	2509
Val	Ser	Leu	Lys	Thr	Gly	Lys	Leu	Asp	Ala	Phe	Ile	Tyr	Asp	Ala	Ala	
							720		725				730			
GTC	TTG	AAT	TAC	AAG	GCT	GGG	AGG	GAT	GAA	GGC	TGC	AAG	CTG	GTG	ACC	2557
Val	Leu	Asn	Tyr	Lys	Ala	Gly	Arg	Asp	Glu	Gly	Cys	Lys	Leu	Val	Thr	
							735		740				745			
ATC	GGG	AGT	GGG	TAC	ATC	TTT	GCC	ACC	ACC	GGT	TAT	GGA	ATT	GCC	CTT	2605
Ile	Gly	Ser	Gly	Tyr	Ile	Phe	Ala	Thr	Thr	Gly	Tyr	Gly	Ile	Ala	Leu	
							750		755				760		765	
CAG	AAA	GGC	TCT	CCT	TGG	AAG	AGG	CAG	ATC	GGC	CTG	GCC	TTG	CTT	CAG	2653
Gln	Lys	Gly	Ser	Pro	Trp	Lys	Arg	Gln	Ile	Asp	Leu	Ala	Leu	Gln		
							770		775				780			
TTT	GTG	GGT	GAT	GGT	GAG	ATG	GAG	GAG	CTG	GAG	ACC	CTG	TGG	CTC	ACT	2701
Phe	Val	Gly	Asp	Gly	Glu	Met	Glu	Glu	Leu	Glu	Thr	Leu	Trp	Leu	Thr	
							785		790				795			
GGG	ATC	TGC	CAC	AAC	GAG	AAG	GAG	GTG	ATG	AGC	AGC	CAG	CTG	GAC		2749
Gly	Ile	Cys	His	Asn	Glu	Lys	Asn	Glu	Val	Met	Ser	Ser	Gln	Leu	Asp	
							800		805				810			
ATT	GAC	AAC	ATG	GCG	GGC	GTA	TTC	TAC	ATG	TTC	GCT	GCC	GCC	ATG	GCC	2797
Ile	Asp	Asn	Met	Ala	Gly	Val	Phe	Tyr	Met	Leu	Ala	Ala	Ala	Met	Ala	
							815		820				825			
CTT	AGC	CTC	ATC	ACC	TTC	ATC	TGG	GAG	CAC	CTG	TTC	TAC	TGG	AAG	CTG	2845
Leu	Ser	Leu	Ile	Thr	Phe	Ile	Trp	Glu	His	Leu	Phe	Tyr	Trp	Lys	Leu	
							830		835				840		845	

CGC TTC TGT TTC ACG GGC GTG TGC TCC GAC CGG CCT GGG TTG CTC TTC	Arg Phe Cys Phe Thr Gly Val Cys Ser Asp Arg Pro Gly Leu Leu Phe	2893	
850	855	860	
TCC ATC AGC AGG GGC ATC TAC AGC TGC ATT CAT GGA GTG CAC ATT GAA	Ser Ile Ser Arg Gly Ile Tyr Ser Cys Ile His Gly Val His Ile Glu	2941	
865	870	875	
GAA AAG AAG AAG TCT CCA GAC TTC AAT CTG ACG GGA TCC CAG AGC AAC	Glu Lys Lys Ser Pro Asp Phe Asn Leu Thr Gly Ser Gln Ser Asn	2989	
880	885	890	
ATG TTA AAA CTC CTC CGG TCA GCC AAA AAC ATT TCC AGC ATG TCC AAC	Met Leu Lys Leu Arg Ser Ala Lys Asn Ile Ser Ser Met Ser Asn	3037	
895	900	905	
ATG AAC TCC TCA AGA ATG GAC TCA CCC AAA AGA GCT GCT GAC TTC ATC	Met Asn Ser Ser Arg Met Asp Ser Pro Lys Arg Ala Ala Asp Phe Ile	3085	
910	915	920	925
CAA AGA GGT TCC CTC ATC ATG GAC ATG GTT TCA GAT AAG GGG AAT TTG	Gln Arg Gly Ser Leu Ile Met Asp Met Val Ser Asp Lys Gly Asn Leu	3133	
930	935	940	
ATG TAC TCA GAC AAC AGG TCC TTT CAG GGG AAA GAG AGC ATT TTT GGA	Met Tyr Ser Asp Asn Arg Ser Phe Gln Gly Lys Glu Ser Ile Phe GLY	3181	
945	950	955	
GAC AAC ATG AAC GAA CTC CAA ACA TTT GTG GCC AAC CGG CAG AAG GAT	Asp Asn Met Asn Glu Leu Gln Thr Phe Val Ala Asn Arg Gln Lys Asp	3229	
960	965	970	
AAC CTC AAT AAC TAT GTA TTC CAG GGA CAA CAT CCT CTT ACT CTC AAT	Asn Leu Asn Asn Tyr Val Phe Gln Gly Gln His Pro Leu Thr Leu Asn	3277	
975	980	985	
GAG TCC AAC CCT AAC ACG GTG GAG GTG GCC GTG AGC ACA GAA TCC AAA	Glu Ser Asn Pro Asn Thr Val Glu Val Ala Val Ser Thr Glu Ser Lys	3325	
990	995	1000	1005
GCG AAC TCT AGA CCC CGG CAG CTG TGG AAG AAA TCC GTG GAT TCC ATA	Ala Asn Ser Arg Pro Arg Gln Leu Trp Lys Lys Ser Val Asp Ser Ile	3373	
1010	1015	1020	
CGC CAG GAT TCA CTA TCC CAG AAT CCA GTC TCC CAG AGG GAT GAG GCA	Arg Gln Asp Ser Leu Ser Gln Asn Pro Val Ser Gln Arg Asp Glu Ala	3421	
1025	1030	1035	
ACA GCA GAS AAT AGG ACC CAC TCC CTA AAG AGC CCT AGG TAT CTT CCA	Thr Ala Glu Asn Arg Thr His Ser Leu Lys Ser Pro Arg Tyr Leu Pro	3469	
1040	1045	1050	
GAA GAG ATG GCC CTC TCT GAC ATT TCA GAA AGG TCA AAT CGG GCC ACG	Glu Glu Met Ala His Ser Asp Ile Ser Glu Thr Ser Asn Arg Ala Thr	3517	
1055	1060	1065	
TGC CAC AGG GAA CCT GAC AAC AGT AAG AAC CAC AAA ACC AAG GAC AAC	Cys His Arg Glu Pro Asp Asn Ser Lys Asn His Lys Thr Lys Asp Asn	3565	
1070	1075	1080	1085
TTT AAA AGG TCA GTG GCC TCC AAA TAC CCC AAG GAC TGT AGT GAG GTC	Phe Lys Arg Ser Val Ala Ser Lys Tyr Pro Lys Asp Cys Ser Glu Val	3613	
1090	1095	1100	
GAG CGC ACC TAC CTG AAA ACC AAA TCA AGC TCC CCT AGA GAC AAG ATC	Glu Arg Thr Tyr Leu Lys Thr Lys Ser Ser Ser Pro Arg Asp Lys Ile	3661	
1105	1110	1115	

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TAC ACT ATA GAT GGT GAG AAG GAG CCT GGT TTC CAC TTA GAT CCA CCC Tyr Thr Ile Asp Gly Glu Lys Glu Pro Gly Phe His Leu Asp Pro Pro 1120 1125 1130	3709
CAG TTT GTT GAA AAT GTG ACC CTG CCC GAG AAC GTG GAC TTC CCG GAC Gln Phe Val Glu Asn Val Thr Leu Pro Glu Asn Val Asp Phe Pro Asp 1135 1140 1145	3757
CCC TAC CAG GAT CCC AGT GAA AAC TTC CGC AAG GGG GAC TCC ACG CTG Pro Tyr Gln Asp Pro Ser Glu Asn Phe Arg Lys Gly Asp Ser Thr Leu 1150 1155 1160 1165	3805
CCA ATG AAC CGG AAC CCC TTG CAT AAT GAA GAG GGG CTT TCC AAC AAC Pro Met Asn Arg Asn Pro Leu His Asn Glu Glu Gly Leu Ser Asn Asn 1170 1175 1180	3853
GAC CAG TAT AAA CTC TAC TCC AAG CAC TTC ACC TTG AAA GAC AAG GGT Asp Gln Tyr Lys Leu Tyr Ser Lys His Phe Thr Leu Lys Asp Lys Gly 1185 1190 1195	3901
TCC CCG CAC AGT GAG ACC AGC GAG CGA TAC CGG CAG AAC TCC ACG CAC Ser Pro His Ser Glu Thr Ser Glu Arg Tyr Arg Gln Asn Ser Thr His 1200 1205 1210	3949
TGC AGA AGC TGC CTT TCC AAC ATG CCC ACC TAT TCA GGC CAC TTC ACC Cys Arg Ser Cys Leu Ser Asn Met Pro Thr Tyr Ser Gly His Phe Thr 1215 1220 1225	3997
ATG AGG TCC CCC TTC AAG TGC GAT GCC TGC CTG CGG ATG GGG AAC CTC Met Arg Ser Pro Phe Lys Cys Asp Ala Cys Leu Arg Met Gly Asn Leu 1230 1235 1240 1245	4045
TAT GAC ATC GAT GAA GAC CAG ATG CTT CAG GAG ACA GGT AAC CCA GCC Tyr Asp Ile Asp Glu Asp Gln Met Leu Gln Glu Thr Gly Asn Pro Ala 1250 1255 1260	4093
ACC GGG GAG CAG GTC TAC CAG CAG GAC TGG GCA CAG AAC AAT GCG CTT Thr Gly Glu Gln Val Tyr Gln Gln Asp Trp Ala Gln Asn Asn Ala Leu 1265 1270 1275	4141
CAA TTA CAA AAG AAC AAG CTA AGG ATT AGC CGT CAG CAT TCC TAC GAT Gln Leu Gln Lys Asn Lys Leu Arg Ile Ser Arg Gln His Ser Tyr Asp 1280 1285 1290	4189
AAC ATT GTC GAC AAA CCT AGG GAG CTA GAC CTT AGC AGG CCC TCC CGG Asn Ile Val Asp Lys Pro Arg Glu Leu Asp Leu Ser Arg Pro Ser Arg 1295 1300 1305	4237
AGC ATA AGC CTC AAG GAC AGG GAA CGG CTT CTG GAG GGA AAT TTT TAC Ser Ile Ser Leu Lys Asp Arg Glu Arg Leu Leu Glu Gly Asn Phe Tyr 1310 1315 1320 1325	4285
GGC AGC CTG TTT AGT GTC CCC TCA AGC AAA CTC TCG GGG AAA AAA AGC Gly Ser Leu Phe Ser Val Pro Ser Ser Lys Leu Ser Gly Lys Lys Ser 1330 1335 1340	4333
TCC CTT TTC CCC CAR GGT CTG GAG GAC AGC AAG AGG AGC AAG TCT CTC Ser Leu Phe Pro Gln Glu Leu Glu Asp Ser Lys Arg Ser Lys Ser Leu 1345 1350 1355	4381
TTG CCA GAC CAC AGC TCC GAT AAC CCT TTC CTC CAC TCC CAC AGG GAT Leu Pro Asp His Thr Ser Asp Asn Pro Phe Leu His Ser His Arg Asp 1360 1365 1370	4429
GAC CAA CGG TTG GTT ATT GGG AGA TGC CCC TCG GAC CCT TAC AAA CAC Asp Gln Arg Leu Val Ile Glu Arg Cys Pro Ser Asp Pro Tyr Lys His 1375 1380 1385	4477

TCG TTG CCA TCC CAG GCG GTG AAT GAC AGC TAT CTT CGG TCG TCC TTG Ser Leu Pro Ser Gln Ala Val Asn Asp Ser Tyr Leu Arg Ser Ser Leu 1390 1395 1400 1405	4525
AGG TCA ACG GCA TCG TAC TGT TCC AGG GAC AGT CGG GGC CAC AAT GAT Arg Ser Thr Ala Ser Tyr Cys Ser Arg Asp Ser Arg Gly His Asn Asp 1410 1415 1420	4573
G TG TAT ATT TCG GAG CAT GTT ATG CCT TAT GCT GCA AAT AAG AAT AAT Val Tyr Ile Ser Glu His Val Met Pro Tyr Ala Ala Asn Lys Asn Asn 1425 1430 1435	4621
ATG TAC TCT ACC CCC AGG GTT TTA AAT TCC TGC AGC AAT AGA CGC GTG Met Tyr Ser Thr Pro Arg Val Leu Asn Ser Cys Ser Asn Arg Arg Val 1440 1445 1450	4669
TAC AAG GAA ATG CCT AGT ATC GAA TCT GAT GTT TAAAAATCTT CCATTAATGT Tyr Lys Glu Met Pro Ser Ile Glu Ser Asp Val 1455 1460 146	4722
TTTATCTATA GGGAAATACA CGTAATGGCC AATGTTCTGG AGGGTAAATG TTGGATGTCC AATAGTGCCC TGCTAAGAGG AAGGAG	4782
	4808

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1464 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Gly Arg Val Gly Tyr Trp Thr Leu Leu Val Leu Pro Ala Leu Leu 1 5 10 15
Val Trp Arg Gly Pro Ala Pro Ser Ala Ala Ala Glu Lys Gly Pro Pro 20 25 30
Ala Leu Asn Ile Ala Val Met Leu Gly His Ser His Asp Val Thr Glu 35 40 45
Arg Glu Leu Arg Thr Leu Trp Gly Pro Glu Gln Ala Ala Gly Leu Pro 50 55 60
Leu Asp Val Asn Val Val Ala Leu Leu Met Asn Arg Thr Asp Pro Lys 65 70 75 80
Ser Leu Ile Thr His Val Cys Asp Leu Met Ser Gly Ala Arg Ile His 85 90 95
Gly Leu Val Phe Gly Asp Asp Thr Asp Gln Glu Ala Val Ala Gln Met 100 105 110
Leu Asp Phe Ile Ser Ser His Thr Phe Val Pro Ile Leu Gly Ile His 115 120 125
Gly Gly Ala Ser Met Ile Met Ala Asp Lys Asp Pro Thr Ser Thr Phe 130 135 140
Phe Gln Phe Gly Ala Ser Ile Gln Gln Ala Thr Val Met Leu Lys 145 150 155 160
Ile Met Gln Asp Tyr Asp Trp His Val Phe Ser Leu Val Thr Thr Ile

165	170	175
Phe Pro Gly Tyr Arg Glu Phe Ile Ser Phe Val Lys Thr Thr Val Asp		
180	185	190
Asn Ser Phe Val Gly Trp Asp Met Gln Asn Val Ile Thr Leu Asp Thr		
195	200	205
Ser Phe Glu Asp Ala Lys Thr Gln Val Gln Leu Lys Lys Ile His Ser		
210	215	220
Ser Val Ile Leu Leu Tyr Cys Ser Lys Asp Glu Ala Val Leu Ile Leu		
225	230	235
240		
Ser Glu Ala Arg Ser Leu Gly Leu Thr Gly Tyr Asp Phe Phe Trp Ile		
245	250	255
Val Pro Ser Leu Val Ser Gly Asn Thr Glu Leu Ile Pro Lys Glu Phe		
260	265	270
Pro Ser Gly Leu Ile Ser Val Ser Tyr Asp Asp Trp Asp Tyr Ser Leu		
275	280	285
Glu Ala Arg Val Arg Asp Gly Ile Gly Ile Leu Thr Thr Ala Ala Ser		
290	295	300
Ser Met Leu Glu Lys Phe Ser Tyr Ile Pro Glu Ala Lys Ala Ser Cys		
305	310	315
320		
Tyr Gly Gln Met Glu Arg Pro Glu Val Pro Met His Thr Leu His Pro		
325	330	335
Phe Met Val Asn Val Thr Trp Asp Gly Lys Asp Leu Ser Phe Thr Glu		
340	345	350
Glu Gly Tyr Gln Val His Pro Arg Leu Val Val Ile Val Leu Asn Lys		
355	360	365
Asp Arg Glu Trp Glu Lys Val Gly Lys Trp Glu Asn His Thr Leu Ser		
370	375	380
Leu Arg His Ala Val Trp Pro Arg Tyr Lys Ser Phe Ser Asp Cys Glu		
385	390	395
400		
Pro Asp Asp Asn His Leu Ser Ile Val Thr Leu Glu Ala Pro Phe		
405	410	415
Val Ile Val Glu Asp Ile Asp Pro Leu Thr Glu Thr Cys Val Arg Asn		
420	425	430
Thr Val Pro Cys Arg Lys Phe Val Lys Ile Asn Asn Ser Thr Asn Glu		
435	440	445
Gly Met Asn Val Lys Lys Cys Cys Lys Gly Phe Cys Ile Asp Ile Leu		
450	455	460
Lys Lys Leu Ser Arg Thr Val Lys Phe Thr Tyr Asp Leu Tyr Leu Val		
465	470	475
480		
485		
490		
495		
Ile Gly Glu Val Val Tyr Gln Arg Ala Val Met Ala Val Gly Ser Leu		
500	505	510
Thr Ile Asn Glu Glu Arg Ser Glu Val Val Asp Phe Ser Val Pro Phe		
515	520	525

Val Glu Thr Gly Ile Ser Val Met Val Ser Arg Ser Asn Gly Thr Val
530 535 540

Ser Pro Ser Ala Phe Leu Glu Pro Phe Ser Ala Ser Val Trp Val Met
545 550 555 560

Met Phe Val Met Leu Leu Ile Val Ser Ala Ile Ala Val Trp Val Leu
565 570 575

Asp Tyr Ser Ser Pro Val Gly Tyr Asn Arg Asn Leu Ala Lys Gly Lys
580 585 590

Ala Pro His Gly Pro Ser Phe Thr Ile Gly Lys Ala Ile Trp Leu Leu
595 600 605

Trp Gly Leu Val Phe Asn Asn Ser Val Pro Val Gln Asn Pro Lys Gly
610 615 620

Thr Thr Ser Lys Ile Met Val Ser Val Trp Ala Phe Phe Ala Val Ile
625 630 635 640

Phe Leu Ala Ser Tyr Thr Ala Asn Leu Ala Ala Phe Met Ile Gln Glu
645 650 655

Glu Phe Val Asp Gln Val Thr Gly Leu Ser Asp Lys Lys Phe Gln Arg
660 665 670

Pro His Asp Tyr Ser Pro Pro Phe Arg Phe Gly Thr Val Pro Asn Gly
675 680 685

Ser Thr Glu Arg Asn Ile Arg Asn Asn Tyr Pro Tyr Met His Gln Tyr
690 695 700

Met Thr Lys Phe Asn Gln Lys Gly Val Glu Asp Ala Leu Val Ser Leu
705 710 715 720

Lys Thr Gly Lys Leu Asp Ala Phe Ile Tyr Asp Ala Ala Val Leu Asn
725 730 735

Tyr Lys Ala Gly Arg Asp Glu Gly Cys Lys Leu Val Thr Ile Gly Ser
740 745 750

Gly Tyr Ile Phe Ala Thr Thr Gly Tyr Gly Ile Ala Leu Gln Lys Gly
755 760 765

Ser Pro Trp Lys Arg Gln Ile Asp Leu Ala Leu Gln Phe Val Gly
770 775 780

Asp Gly Glu Met Glu Glu Leu Glu Thr Leu Trp Leu Thr Gly Ile Cys
785 790 795 800

His Asn Glu Lys Asn Glu Val Met Ser Ser Gln Leu Asp Ile Asp Asn
805 810 815

Met Ala Gly Val Phe Tyr Met Leu Ala Ala Ala Met Ala Leu Ser Leu
820 825 830

Ile Thr Phe Ile Trp Glu His Leu Phe Tyr Trp Lys Leu Arg Phe Cys
835 840 845

Phe Thr Gly Val Cys Ser Asp Arg Pro Gly Leu Leu Phe Ser Ile Ser
850 855 860

Arg Gly Ile Tyr Ser Cys Ile His Gly Val His Ile Glu Glu Lys Lys
865 870 875 880

Lys Ser Pro Asp Phe Asn Leu Thr Gly Ser Gln Ser Asn Met Leu Lys

885	890	895
Leu Leu Arg Ser Ala Lys Asn Ile Ser Ser Met Ser Asn Met Asn Ser 900	905	910
Ser Arg Met Asp Ser Pro Lys Arg Ala Ala Asp Phe Ile Gln Arg Gly 915	920	925
Ser Leu Ile Met Asp Met Val Ser Asp Lys Gly Asn Leu Met Tyr Ser 930	935	940
Asp Asn Arg Ser Phe Gln Gly Lys Glu Ser Ile Phe Gly Asp Asn Met 945	950	955
Asn Glu Leu Gln Thr Phe Val Ala Asn Arg Gln Lys Asp Asn Leu Asn 965	970	975
Asn Tyr Val Phe Gln Gly Gln His Pro Leu Thr Leu Asn Glu Ser Asn 980	985	990
Pro Asn Thr Val Glu Val Ala Val Ser Thr Glu Ser Lys Ala Asn Ser 995	1000	1005
Arg Pro Arg Gln Leu Trp Lys Lys Ser Val Asp Ser Ile Arg Gln Asp 1010	1015	1020
Ser Leu Ser Gln Asn Pro Val Ser Gln Arg Asp Glu Ala Thr Ala Glu 1025	1030	1035
Asn Arg Thr His Ser Leu Lys Ser Pro Arg Tyr Leu Pro Glu Glu Met 1045	1050	1055
Ala His Ser Asp Ile Ser Glu Thr Ser Asn Arg Ala Thr Cys His Arg 1060	1065	1070
Glu Pro Asp Asn Ser Lys Asn His Lys Thr Lys Asp Asn Phe Lys Arg 1075	1080	1085
Ser Val Ala Ser Lys Tyr Pro Lys Asp Cys Ser Glu Val Glu Arg Thr 1090	1095	1100
Tyr Leu Lys Thr Lys Ser Ser Pro Arg Asp Lys Ile Tyr Thr Ile 1105	1110	1115
Asp Gly Glu Lys Glu Pro Gly Phe His Leu Asp Pro Pro Gln Phe Val 1125	1130	1135
Glu Asn Val Thr Leu Pro Glu Asn Val Asp Phe Pro Asp Pro Tyr Gln 1140	1145	1150
Asp Pro Ser Glu Asn Phe Arg Lys Gly Asp Ser Thr Leu Pro Met Asn 1155	1160	1165
Arg Asn Pro Leu His Asn Glu Glu Gly Leu Ser Asn Asn Asp Gln Tyr 1170	1175	1180
Lys Leu Tyr Ser Lys His Phe Thr Leu Lys Asp Lys Gly Ser Pro His 1185	1190	1195
Ser Glu Thr Ser Glu Arg Tyr Arg Gln Asn Ser Thr His Cys Arg Ser 1205	1210	1215
Cys Leu Ser Asn Met Pro Thr Tyr Ser Gly His Phe Thr Met Arg Ser 1220	1225	1230
Pro Phe Lys Cys Asp Ala Cys Leu Arg Met Gly Asn Leu Tyr Asp Ile 1235	1240	1245

Asp Glu Asp Gln Met Leu Gln Glu Thr Gly Asn Pro Ala Thr Gly Glu
1250 1255 1260

Gln Val Tyr Gln Gln Asp Trp Ala Gln Asn Ala Leu Gln Leu Gln
1265 1270 1275 1280

Lys Asn Lys Leu Arg Ile Ser Arg Gln His Ser Tyr Asp Asn Ile Val
1285 1290 1295

Asp Lys Pro Arg Glu Leu Asp Leu Ser Arg Pro Ser Arg Ser Ile Ser
1300 1305 1310

Leu Lys Asp Arg Glu Arg Leu Leu Glu Gly Asn Phe Tyr Gly Ser Leu
1315 1320 1325

Phe Ser Val Pro Ser Ser Lys Leu Ser Gly Lys Lys Ser Ser Leu Phe
1330 1335 1340

Pro Gln Gly Leu Glu Asp Ser Lys Arg Ser Lys Ser Leu Leu Pro Asp
1345 1350 1355 1360

His Thr Ser Asp Asn Pro Phe Leu His Ser His Arg Asp Asp Gln Arg
1365 1370 1375

Leu Val Ile Gly Arg Cys Pro Ser Asp Pro Tyr Lys His Ser Leu Pro
1380 1385 1390

Ser Gln Ala Val Asn Asp Ser Tyr Leu Arg Ser Ser Leu Arg Ser Thr
1395 1400 1405

Ala Ser Tyr Cys Ser Arg Asp Ser Arg Gly His Asn Asp Val Tyr Ile
1410 1415 1420

Ser Glu His Val Met Pro Tyr Ala Ala Asn Lys Asn Asn Met Tyr Ser
1425 1430 1435 1440

Thr Pro Arg Val Leu Asn Ser Cys Ser Asn Arg Arg Val Tyr Lys Glu
1445 1450 1455

Met Pro Ser Ile Glu Ser Asp Val
1460

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 74 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CGAGGGAGGC GGCGGGCGCG GACTCTCTTC GCAGGGCGCAG CGCCCGTTCC CCCTCGGACC 60
CTCCGGTGGA CATG 74

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3155 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: both
(D) TOPOLOGY both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 262..3030

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CAAGCCGGGC GTTCGGAGCT GTGCCCGGCG CGCTTCAGC ACCGCGGACA GCGCCGGCCG	60
CGTGGGGCTG AGCGCCGAGC CCCCAGCGACG CTTCAGCCC CCCTTCCTC GGCGGACGTC	120
CCGGGACCGC CGCTCCGGGG GAGACGTGGC GTCCCGAGCC CGCGGGGCCG GGCGAGCGCA	180
GGACGGCCCG GAAGCCCCGC GGGGGATCTG CGAGGGCCG CGCGTTGCGC CCGCGCAGAG	240
CCAGGCCCGC GGCCCGAGCC C ATG AGC ACC ATG CGC CTG CTG ACG CTC GCC	291
Met Ser Thr Met Arg Leu Leu Thr Leu Ala	
1 5 10	
CTG CTG TTC TCC TCC GTC GGC CGT GGC GCG TGC GAC CCC AAG ATC	339
Leu Leu Phe Ser Cys Ser Val Ala Arg Ala Ala Cys Asp Pro Lys Ile	
15 20 25	
GTC AAC ATT GGC GCG GTG CTG AGC ACG CGG AAG CAC GAG CAG ATG TTC	387
Val Asn Ile Gly Ala Val Leu Ser Thr Arg Lys His Glu Gln Met Phe	
30 35 40	
CGC GAG GCC GTG AAC CAG GCG AAC AAG CGG CAC GGC TCC TGG AAG ATT	435
Arg Glu Ala Val Asn Gln Ala Asn Lys Arg His Gly Ser Trp Lys Ile	
45 50 55	
CAG CTC AAT GCC ACC TCC GTC ACC CAC AAG CCC AAC GCG ATC CAG ATG	483
Gln Leu Asn Ala Thr Ser Val Thr His Lys Pro Asn Ala Ile Gln Met	
60 65 70	
GCT CTG TCG GTG TGC GAG GAC CTC ATC TCC AGC CAG GTC TAC GCC ATC	531
Ala Leu Ser Val Cys Glu Asp Leu Ile Ser Ser Gln Val Tyr Ala Ile	
75 80 85 90	
CTA GTT AGC CAT CCT ACC CCC AAC GAC CAC TTC ACT CCC ACC CCT	579
Leu Val Ser His Pro Pro Thr Pro Asn Asp His Phe Thr Pro Thr Pro	
95 100 105	
GTC TCC TAC ACA GCG GGC TTC TAC CGC ATA CCC GTG CTG GGG CTG ACC	627
Val Ser Tyr Thr Ala Gly Phe Tyr Arg Ile Pro Val Leu Gly Leu Thr	
110 115 120	
ACC CGC ATG TCC ATC TAC TCG GAC AAG AGC ATC CAC CTG AGC TTC CTG	675
Thr Arg Met Ser Ile Tyr Ser Asp Lys Ser Ile His Leu Ser Phe Leu	
125 130 135	
CGC ACC GTG CCG CCC TAC TCC CAC CAG TCC AGC GTG TGG TTT GAG ATG	723
Arg Thr Val Pro Pro Tyr Ser His Gln Ser Ser Val Trp Phe Glu Met	
140 145 150	
ATG CGT GTC TAC AGC TGG AAC CAC ATC ATC CTG CTG GTC AGC GAC GAC	771
Met Arg Val Tyr Ser Trp Asn His Ile Ile Leu Leu Val Ser Asp Asp	
155 160 165 170	
CAT GAG GGC CGG GCG GCT CAG AAA CGC CTG GAG ACG CTG CTG GAG GAG	819
His Glu Gly Arg Ala Ala Gln Lys Arg Leu Glu Thr Leu Leu Glu Glu	

175	180	185	
CGT GAS TCC AAG GCA GAG AAG GTG CTG CAG TTT GAC CCA GGG ACC AAG Arg Glu Ser Lys Ala Glu Lys Val Leu Gin Phe Asp Pro Gly Thr Lys 190 195 200			867
AAC GTG ACG GCC CTG CTG ATG GAG GCG AAA GAG CTG GAG GCC CGG GTC Asn Val Thr Ala Leu Leu Met Glu Ala Lys Glu Leu Glu Ala Arg Val 205 210 215			915
ATC ATC CTT TCT GCC AGC GAG GAC GAT GCT GCC ACT STA TAC CGC GCA Ile Ile Leu Ser Ala Ser Glu Asp Asp Ala Ala Thr Val Tyr Arg Ala 220 225 230			963
GCC GCG ATG CTG AAC ATG ACG GGC TCC GGG TAC GTG TGG CTG GTC GGC Ala Ala Met Leu Asn Met Thr Gly Ser Gly Tyr Val Trp Leu Val Gly 235 240 245 250			1011
GAG CGC GAG ATC TCG GGG AAC GCC CTG CGC TAC GCC CCA GAC GGC ATC Glu Arg Glu Ile Ser Gly Asn Ala Leu Arg Tyr Ala Pro Asp Gly Ile 255 260 265			1059
CTC GGG CTG CAG CTC ATC AAC GGC AAG AAC GAG TCG GCC CAC ATC AGC Leu Gly Leu Gln Leu Ile Asn Gly Lys Asn Glu Ser Ala His Ile Ser 270 275 280			1107
GAC GCC GTG GGC GTG GTG GCC CAG GCC GTG CAC GAG CTC CTC GAG AAG Asp Ala Val Gly Val Val Ala Gln Ala Val His Glu Leu Leu Glu Lys 285 290 295			1155
GAG AAC ATC ACC GAC CCG CCG CGG GGC TGC GTG GGC AAC ACC AAC ATC Glu Asn Ile Thr Asp Pro Pro Arg Gly Cys Val Gly Asn Thr Asn Ile 300 305 310			1203
TGG AAG ACC GGG CCG CTC TTC AAG AGA GTG CTG ATG TCT TCC AAG TAT Trp Lys Thr Gly Pro Leu Phe Lys Arg Val Leu Met Ser Ser Lys Tyr 315 320 325 330			1251
GCG GAT GGG GTG ACT GGT CGC GTG GAG TTC AAT GAG GAT GGG GAC CGG Ala Asp Gly Val Thr Gly Arg Val Glu Phe Asn Glu Asp Gly Asp Arg 335 340 345			1299
AAG TTC GCC AAC TAC AGC ATC ATG AAC CTG CAG AAC CGC AAG CTG GTG Lys Phe Ala Asn Tyr Ser Ile Met Asn Leu Gln Asn Arg Lys Leu Val 350 355 360			1347
CAA GTG GGC ATC TAC AAT GGC ACC CAC GTC ATC CCT AAT GAC AGG AAG Gln Val Gly Ile Tyr Asn Gly Thr His Val Ile Pro Asn Asp Arg Lys 365 370 375			1395
ATC ATC TGG CCA GGC GGA GAG ACA GAG AAG CCT CGA GGG TAC CAG ATG Ile Ile Trp Pro Gly Gly Glu Thr Glu Lys Pro Arg Gly Tyr Gln Met 380 385 390			1443
TCC ACC AGA CTG AAG ATT GTG ACG ATC CAC CAG GAG CCC TTC GTG TAC Ser Thr Arg Leu Lys Ile Val Thr Ile His Gln Glu Pro Phe Val Tyr 395 400 405 410			1491
GTC AAG CCC ACG CTG AGT GAT GGG ACA TGC AAG GAG GAG TTC ACA GTC Val Lys Pro Thr Leu Ser Asp Gly Thr Cys Lys Glu Glu Phe Thr Val 415 420 425			1539
AAC GGC GAC CCA GTC AAG AAG GTG ATC TGC ACC GGG CCC AAC GAC ACG Asn Gly Asp Pro Val Lys Lys Val Ile Cys Thr Gly Pro Asn Asp Thr 430 435 440			1587

TCG CCG GGC AGC CCC CGC CAC ACG GTG CCT CAG TGT TGC TAC GGC TTT Ser Pro Gly Ser Pro Arg His Thr Val Pro Gln Cys Cys Tyr Gly Phe 445 450 455	1635
TGC ATC GAC CTG CTC ATC AAG CTG GCA CGG ACC ATG AAC TTC ACC TAC Cys Ile Asp Leu Leu Ile Lys Leu Ala Arg Thr Met Asn Phe Thr Tyr 460 465 470	1683
GAG GTG CAC CTG GTG GCA GAT GGC AAG TTC GGC ACA CAG GAG CGG GTG Glu Val His Leu Val Ala Asp Gly Lys Phe Gly Thr Gln Glu Arg Val 475 480 485 490	1731
AAC AAC AGC AAC AAG AAG GAG TGG AAT GGG ATG ATG GGC GAG CTG CTC Asn Asn Ser Asn Lys Lys Glu Trp Asn Gly Met Met Gly Glu Leu Leu 495 500 505	1779
AGC GGG CAG GCA GAC ATG ATC GTG GCG CCG CTA ACC ATA AAC AAC GAG Ser Gly Gln Ala Asp Met Ile Val Ala Pro Leu Thr Ile Asn Asn Glu 510 515 520	1827
CGC GCG CAG TAC ATC GAG TTT TCC AAG CCG TTC AAG TAC CAG GGC CTG Arg Ala Gln Tyr Ile Glu Phe Ser Lys Pro Phe Lys Tyr Gln Gly Leu 525 530 535	1875
ACT ATT CTG GTC AAG AAG GAG ATT CCC CGG AGC ACG CTG GAC TCG TTC Thr Ile Leu Val Lys Lys Glu Ile Pro Arg Ser Thr Leu Asp Ser Phe 540 545 550	1923
ATG CAG CCG TTC CAG AGC ACA CTG TGG CTG CTG GTG GGC CTG TCG GTG Met Gln Pro Phe Gln Ser Thr Leu Trp Leu Val Gly Leu Ser Val 555 560 565 570	1971
CAC GTG GTG GCC GTG ATG CTG TAC CTG CTG GAC CGC TTC AGC CCC TTC His Val Val Ala Met Leu Tyr Leu Leu Asp Arg Phe Ser Pro Phe 575 580 585	2019
GGC CGG TTC AAG GTG AAC AGC GAG GAG GAG GAG GAC GCA CTG ACC Gly Arg Phe Lys Val Asn Ser Glu Glu Glu Glu Asp Ala Leu Thr 590 595 600	2067
CTG TCC TCG GCC ATG TGG TTC TCC TGG GGC GTC CTG CTC AAC TCC GGC Leu Ser Ser Ala Met Trp Phe Ser Trp Gly Val Leu Leu Asn Ser Gly 605 610 615	2115
ATC GGG GAA GGC GCC CCC AGA AGC TTC TCA GCG CGC ATC CTG GGC ATG Ile Gly Glu Gly Ala Pro Arg Ser Phe Ser Ala Arg Ile Leu Gly Met 620 625 630	2163
GTG TGG GCC GGC TTT GCC ATG ATC ATC GTG GCC TCC TAC ACC GGC AAC Val Trp Ala Gly Phe Ala Met Ile Ile Val Ala Ser Tyr Thr Ala Asn 635 640 645 650	2211
CTG GCG GCC TTC CTG GTG CTG GAC CGG CCG GAG GAG CGC ATC ACG GGC Leu Ala Ala Phe Leu Val Leu Asp Arg Pro Glu Glu Arg Ile Thr Gly 655 660 665	2259
ATC AAC GAC CCT CGG CTG AGG AAC CCC TCG GAC AAG TTT ATC TAC GCC Ile Asn Asp Pro Arg Ile Arg Asn Pro Ser Asp Lys Phe Ile Tyr Ala 670 675 680	2307
ACG GTG AAG CAG AGC TCC GTG GAT ATC TAC TTC CGG CGC CAG GTG GAG Thr Val Lys Gln Ser Ser Val Asp Ile Tyr Phe Arg Arg Gln Val Glu 685 690 695	2355
CTG AGC ACC ATG TAC CGG CAT ATG GAG AAG CAC AAC TAG GAG AGT GCG Leu Ser Thr Met Tyr Arg His Met Glu Lys His Asn Tyr Gln Ser Ala 700 705 710	2403

GCG GAG GGC ATC CAS GCC GTG AGA GAC AAC AAG CTG CAT GCC TTC ATC Ala Glu Ala Ile Gln Ala Val Arg Asp Asn Lys Leu His Ala Phe Ile	2451
715 720 725 730	
TGG GAC TCG GCG GTG CTG GAG TTC GAG GCC TCG CAG AAG TGC GAC CTG Trp Asp Ser Ala Val Leu Glu Phe Glu Ala Ser Gln Lys Cys Asp Leu	2499
735 740 745	
GTG ACG ACT GGA GAG CTG TTT TTC CGC TCG GGC TTC GGC ATA GGC ATG Val Thr Thr Gly Glu Leu Phe Phe Arg Ser Gly Phe Gly Ile Gly Met	2547
750 755 760	
CGC AAA GAC AGC CCC TGG AAG CAG AAC GTC TCC CTG TCC ATC CTC AAG Arg Lys Asp Ser Pro Trp Lys Gln Asn Val Ser Leu Ser Ile Leu Lys	2595
765 770 775	
TCC CAC GAG AAT GGC TTC ATG GAA GAC CTG GAC AAG ACG TGG GTT CGG Ser His Glu Asn Gly Phe Met Glu Asp Leu Asp Lys Thr Trp Val Arg	2643
780 785 790	
TAT CAG GAA TGT GAC TCG CGC AGC AAC GCC CCT GCG ACC CTT ACT TTT Tyr Gln Glu Cys Asp Ser Arg Ser Asn Ala Pro Ala Thr Leu Thr Phe	2691
795 800 805 810	
GAG AAC ATG GCC GGG GTG TTC ATG CTG GTA GCT GGG GGC ATC GTG GCC Glu Asn Met Ala Gly Val Phe Met Leu Ala Gly Gly Ile Val Ala	2739
815 820 825	
GGG ATC TTC CTG ATT TTC ATC GAS ATT GCC TAC AAG CGG CAC AAG GAT Gly Ile Phe Leu Ile Phe Ile Glu Ile Ala Tyr Lys Arg His Lys Asp	2787
830 835 840	
GCT CGC CGG AAG CAG ATG CAG CTG GCC TTT GCC GCC GTT AAC GTG TGG Ala Arg Arg Lys Gln Met Gln Leu Ala Phe Ala Ala Val Asn Val Trp	2835
845 850 855	
CGG AAG AAC CTG CAG GAT AGA AAG AGT GGT AGA GCA GAG CCT GAC CCT Arg Lys Asn Leu Gln Asp Arg Lys Ser Gly Arg Ala Glu Pro Asp Pro	2883
860 865 870	
AAA AAG AAA GCC ACA TTT AGG GCT ATC ACC TCC ACC CTG GCT TCC AGC Lys Lys Lys Ala Thr Phe Arg Ala Ile Thr Ser Thr Leu Ala Ser Ser	2931
875 880 885 890	
TTC AAG AGG CGT AGG TCC TCC AAA GAC ACG CAG TAC CAT CCC ACT GAT Phe Lys Arg Arg Ser Ser Lys Asp Thr Gln Tyr His Pro Thr Asp	2979
895 900 905	
ATC ACG GGC CGG CTC AAC CTC TCA GAT CCC TCG GTC AGC ACC GTG GTG Ile Thr Gly Pro Leu Asn Leu Ser Asp Pro Ser Val Ser Thr Val Val	3027
910 915 920	
TGAGGCCCGG GGAGGGCGCC ACCTGCCAG TTAGCCCCGGC CAAGGACACT GATGGGTGCT	3087
GCTGCTCGGG AAGGCCTGAG GGAAGCCAC CCGCCCCAGA GACTGCCAC CCTGGGCCTC	3147
CCGTCCGT	3155

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 922 amino acids
(B) TYPE: amino acid
(C) TOPOLOGY: linear
(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met Ser Thr Met Arg Leu Leu Thr Leu Ala Leu Leu Phe Ser Cys Ser
1 5 10 15

Val Ala Arg Ala Ala Cys Asp Pro Lys Ile Val Asn Ile Gly Ala Val
20 25 30

Leu Ser Thr Arg Lys His Glu Gln Met Phe Arg Glu Ala Val Asn Gln
35 40 45

Ala Asn Lys Arg His Gly Ser Trp Lys Ile Gln Leu Asn Ala Thr Ser
50 55 60

Val Thr His Lys Pro Asn Ala Ile Gln Met Ala Leu Ser Val Cys Glu
65 70 75 80

Asp Leu Ile Ser Ser Gln Val Tyr Ala Ile Leu Val Ser His Pro Pro
85 90 95

Thr Pro Asn Asp His Phe Thr Pro Val Ser Tyr Thr Ala Gly
100 105 110

Phe Tyr Arg Ile Pro Val Leu Gly Leu Thr Thr Arg Met Ser Ile Tyr
115 120 125

Ser Asp Lys Ser Ile His Leu Ser Phe Leu Arg Thr Val Pro Pro Tyr
130 135 140

Ser His Gln Ser Ser Val Trp Phe Glu Met Met Arg Val Tyr Ser Trp
145 150 155 160

Asn His Ile Ile Leu Leu Val Ser Asp Asp His Glu Gly Arg Ala Ala
165 170 175

Gln Lys Arg Leu Glu Thr Leu Leu Glu Glu Arg Glu Ser Ala Glu
180 185 190

Lys Val Leu Gln Phe Asp Pro Gly Thr Lys Asn Val Thr Ala Leu Leu
195 200 205

Met Glu Ala Lys Glu Leu Glu Ala Arg Val Ile Ile Leu Ser Ala Ser
210 215 220

Glu Asp Asp Ala Ala Thr Val Tyr Arg Ala Ala Met Leu Asn Met
225 230 235 240

Thr Gly Ser Gly Tyr Val Trp Leu Val Gly Glu Arg Glu Ile Ser Gly
245 250 255

Asn Ala Leu Arg Tyr Ala Pro Asp Gly Ile Leu Gly Leu Gln Leu Ile
260 265 270

Asn Gly Lys Asn Glu Ser Ala His Ile Ser Asp Ala Val Gly Val Val
275 280 285

Ala Gln Ala Val His Glu Leu Leu Glu Lys Glu Asn Ile Thr Asp Pro
290 295 300

Pro Arg Gly Cys Val Gly Asn Thr Asn Ile Trp Lys Thr Gly Pro Leu
305 310 315 320

Phe Lys Arg Val Leu Met Ser Ser Lys Tyr Ala Asp Gly Val Thr Gly
325 330 335

Arg Val Glu Phe Asn Glu Asp Gly Asp Arg Lys Phe Ala Asn Tyr Ser
340 345 350

Ile Met Asn Leu Gln Asn Arg Lys Ile Val Gln Val Gly Ile Tyr Asn
355 360 365

Gly Thr His Val Ile Pro Asn Asp Arg Lys Ile Ile Trp Pro Gly Gly
370 375 380 385

Glu Thr Glu Lys Pro Arg Gly Tyr Gln Met Ser Thr Arg Leu Lys Ile
385 390 395 400

Val Thr Ile His Gln Glu Pro Phe Val Tyr Val Lys Pro Thr Leu Ser
405 410 415

Asp Gly Thr Cys Lys Glu Glu Phe Thr Val Asn Gly Asp Pro Val Lys
420 425 430

Lys Val Ile Cys Thr Gly Pro Asn Asp Thr Ser Pro Gly Ser Pro Arg
435 440 445

His Thr Val Pro Gln Cys Cys Tyr Gly Phe Cys Ile Asp Leu Leu Ile
450 455 460

Lys Leu Ala Arg Thr Met Asn Phe Thr Tyr Glu Val His Leu Val Ala
465 470 475 480

Asp Gly Lys Phe Gly Thr Gln Glu Arg Val Asn Asn Ser Asn Lys Lys
485 490 495

Glu Trp Asn Gly Met Met Gly Glu Leu Leu Ser Gly Gln Ala Asp Met
500 505 510

Ile Val Ala Pro Leu Thr Ile Asn Asn Glu Arg Ala Gln Tyr Ile Glu
515 520 525

Phe Ser Lys Pro Phe Lys Tyr Gln Gly Leu Thr Ile Leu Val Lys Lys
530 535 540

Glu Ile Pro Arg Ser Thr Leu Asp Ser Phe Met Gln Pro Phe Gln Ser
545 550 555 560

Thr Leu Trp Leu Leu Val Gly Leu Ser Val His Val Val Ala Val Met
565 570 575

Leu Tyr Leu Leu Asp Arg Phe Ser Pro Phe Gly Arg Phe Lys Val Asn
580 585 590

Ser Glu Glu Glu Glu Asp Ala Leu Thr Leu Ser Ser Ala Met Trp
595 600 605

Phe Ser Trp Gly Val Leu Leu Asn Ser Gly Ile Gly Glu Gly Ala Pro
610 615 620

Arg Ser Phe Ser Ala Arg Ile Leu Gly Met Val Trp Ala Gly Phe Ala
625 630 635 640

Met Ile Ile Val Ala Ser Tyr Thr Ala Asn Leu Ala Ala Phe Leu Val
645 650 655

Leu Asp Arg Pro Glu Glu Arg Ile Thr Gly Ile Asn Asp Pro Arg Leu
660 665 670

Arg Asn Pro Ser Asp Lys Phe Ile Tyr Ala Thr Val Lys Gln Ser Ser
675 680 685

Val Asp Ile Tyr Phe Arg Arg Gln Val Glu Leu Ser Thr Met Tyr Arg
690 695 700

His Met Glu Lys His Asn Tyr Glu Ser Ala Ala Glu Ala Ile Gln Ala
705 710 715 720

Val Arg Asp Asn Lys Leu His Ala Phe Ile Trp Asp Ser Ala Val Leu
725 730 735

Glu Phe Glu Ala Ser Gln Lys Cys Asp Leu Val Thr Thr Gly Glu Leu
740 745 750

Phe Phe Arg Ser Gly Phe Gly Ile Gly Met Arg Lys Asp Ser Pro Trp
755 760 765

Lys Gln Asn Val Ser Leu Ser Ile Leu Lys Ser His Glu Asn Gly Phe
770 775 780

Met Glu Asp Leu Asp Lys Thr Trp Val Arg Tyr Gln Glu Cys Asp Ser
785 790 795 800

Arg Ser Asn Ala Pro Ala Thr Leu Thr Phe Glu Asn Met Ala Gly Val
805 810 815

Phe Met Leu Val Ala Gly Gly Ile Val Ala Gly Ile Phe Leu Ile Phe
820 825 830

Ile Glu Ile Ala Tyr Lys Arg His Lys Asp Ala Arg Arg Lys Gln Met
835 840 845

Gln Leu Ala Phe Ala Ala Val Asn Val Trp Arg Lys Asn Leu Gln Asp
850 855 860

Arg Lys Ser Gly Arg Ala Glu Pro Asp Pro Lys Lys Lys Ala Thr Phe
865 870 875 880

Arg Ala Ile Thr Ser Thr Leu Ala Ser Ser Phe Lys Arg Arg Arg Ser
885 890 895

Ser Lys Asp Thr Gln Tyr His Pro Thr Asp Ile Thr Gly Pro Leu Asn
900 905 910

Leu Ser Asp Pro Ser Val Ser Thr Val Val
915 920

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2540 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..2334

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

AAC GAC CAC TTC ACT CCC ACC CCT GTC TCC TAC ACA GCC GGC TTC TAC
Asn Asp His Phe Thr Pro Thr Pro Val Ser Tyr Thr Ala Gly Phe Tyr
1 5 10 15

CGG ATA CCC GTG CTG GGG CTG ACC ACC CGC ATG TCC ATC TAC TCG GAC

48

96

Arg Ile Pro Val Leu Gly Leu Thr Thr Arg Met Ser Ile Tyr Ser Asp			
20 25 30			
AAG AGC ATC CAC CTG AGC TTC CTG CGC ACC GTG CCG CCC TAC TCC CAC			144
Lys Ser Ile His Leu Ser Phe Leu Arg Thr Val Pro Pro Tyr Ser His			
35 40 45			
CAG TCC AGC GTG TGG TTT GAG ATG ATG CGT GTC TAC AGC TGG AAC CAC			192
Gln Ser Ser Val Trp Phe Glu Met Met Arg Val Tyr Ser Trp Asn His			
50 55 60			
ATC ATC CTG CTG GTG AGC GAC CAC GAG GGC CGG GCG GCT CAG AAA			240
Ile Ile Leu Leu Val Ser Asp Asp His Glu Gly Arg Ala Ala Gln Lys			
65 70 75 80			
CGC CTG GAG ACG CTG CTG GAG GAG CGT GAG TCC AAG AGT AAA AAA AGG			288
Arg Leu Glu Thr Leu Leu Glu Arg Glu Ser Lys Ser Lys Lys Arg			
85 90 95			
AAC TAT GAA AAC CTC GAC CAA CTG TCC TAT GAC AAC AAG CGC GGA CCC			336
Asn Tyr Glu Asn Leu Asp Gln Leu Ser Tyr Asp Asn Lys Arg Gly Pro			
100 105 110			
AAG GCA GAG AAG GTG CTG CAG TTT GAC CCA GGG ACC AAG AAC GTG ACG			384
Lys Ala Glu Lys Val Leu Gln Phe Asp Pro Gly Thr Lys Asn Val Thr			
115 120 125			
GCC CTG CTG ATG GAG GCG AAA GAG CTG GAG GCC CGG GTC ATC ATC CTT			432
Ala Leu Leu Met Glu Ala Lys Glu Leu Glu Ala Arg Val Ile Ile Leu			
130 135 140			
TCT GCC AGC GAG GAC GAT GCT GCC ACT GTA TAC CGC GCA GCC GCG ATG			480
Ser Ala Ser Glu Asp Asp Ala Ala Thr Val Tyr Arg Ala Ala Ala Met			
145 150 155 160			
CTG AAC ATG ACG GGC AAC ACC AAC ATC TGG AAG ACC GGG CCG CTC TTC			528
Leu Asn Met Thr Gly Asn Thr Asn Ile Trp Lys Thr Gly Pro Leu Phe			
165 170 175			
AAG AGA GTG CTG ATG TCT TCC AAG TAT GCG GAT GGG GTG ACT GGT CGC			576
Lys Arg Val Leu Met Ser Ser Lys Tyr Ala Asp Gly Val Thr Gly Arg			
180 185 190			
GTG GAG TTC AAT GAG GAT GGG GAC CGG AAG TTC GCC AAC TAC AGC ATC			624
Val Glu Phe Asn Glu Asp Gly Asp Arg Lys Phe Ala Asn Tyr Ser Ile			
195 200 205			
ATG AAC CTG CAG AAC CGC AAG CTG GTG CAA GTG GGC ATC TAC AAT GGC			672
Met Asn Leu Gln Asn Arg Lys Leu Val Gln Val Gly Ile Tyr Asn Glu			
210 215 220			
ACC CAT GTG ATC CCT AAT GAC AGG AAG ATC ATC TGG CCA GGC GGA GAG			720
Thr His Val Ile Pro Asn Asp Arg Lys Ile Ile Trp Pro Gly Gly Glu			
225 230 235 240			
ACA GAG AAG CCT CGA GGG TAC CAG ATG TCC ACC AGA CTG AAG ATT GTG			768
Thr Glu Lys Pro Arg Gly Tyr Gln Met Ser Thr Arg Leu Lys Ile Val			
245 250 255			
ACG ATC CAC CAG GAG CCC TTC GTG TAC GTC AAG CCC ACG CTG AGT GAT			816
Thr Ile His Gln Glu Pro Phe Val Tyr Val Lys Pro Thr Leu Ser Asp			
260 265 270			
GGG ACA TGC AAG GAG GAG TTC ACA GTC AAC GGC GAC CCA GTC AAG AAG			864
Gly Thr Cys Lys Glu Glu Phe Thr Val Asn Gly Asp Pro Val Lys Lys			
275 280 285			

GTG ATC TGC ACC GGG CCC AAC GAC ACG TCG CCG GGC AGC CCC CGC CAC	912
Val Ile Cys Thr Gly Pro Asn Asp Thr Ser Pro Gly Ser Pro Arg His	
290 295 300	
ACG GTG CCT CAG TGT TGC TAC GGC TTT TGC ATC GAC CTG CTC ATC AAG	963
Thr Val Pro Gln Cys Cys Tyr Gly Phe Cys Ile Asp Leu Leu Ile Lys	
305 310 315 320	
CTG GCA CGG ACC ATG AAC TTC ACC TAC GAG GTG CAC CTG GTG GCA GAT	1008
Leu Ala Arg Thr Met Asn Phe Thr Tyr Glu Val His Leu Val Ala Asp	
325 330 335	
GGC AAG TTC GGC ACA CAG GAG CGG GTG AAC AAC AGC AAC AAG AAG GAG	1056
Gly Lys Phe Gly Thr Gln Glu Arg Val Asn Asn Ser Asn Lys Lys Glu	
340 345 350	
TGG AAT GGG ATG ATG GGC GAG CTG CTC AGC GGG CAG GCA GAC ATG ATC	1104
Trp Asn Gly Met Met Gly Glu Leu Leu Ser Gly Gln Ala Asp Met Ile	
355 360 365	
GTG GCG CGG CTA ACC ATA AAC AAC GAG CGC GCG CAG TAC ATC GAG TTT	1152
Val Ala Pro Leu Thr Ile Asn Asn Glu Arg Ala Gln Tyr Ile Glu Phe	
370 375 380	
TCC AAG CCC TTC AAG TAC CAG GGC CTG ACT ATT CTG GTC AAG AAG GAG	1200
Ser Lys Pro Phe Lys Tyr Gln Gly Leu Thr Ile Leu Val Lys Lys Glu	
385 390 395 400	
ATT CCC CGG AGC ACG CTG GAC TCG TTC ATG CAG CCG TTC CAG AGC ACA	1248
Ile Pro Arg Ser Thr Leu Asp Ser Phe Met Gln Pro Phe Gln Ser Thr	
405 410 415	
CTG TGG CTG CTG GTG GGG CTG TCG GTG CAC GTG GTG GCC GTG ATG CTG	1295
Leu Trp Leu Leu Val Gly Leu Ser Val His Val Val Ala Val Met Leu	
420 425 430	
TAC CTG CTG GAC CGC TTC AGC CCC TTC GGC CGG TTC AAG GTG AAC AGC	1344
Tyr Leu Leu Asp Arg Phe Ser Pro Phe Gly Arg Phe Lys Val Asn Ser	
435 440 445	
GAG GAG GAG GAG GAC GCA CTG ACC CTG TCC TCG GCC ATG TGG TTC	1392
Glu Glu Glu Glu Asp Ala Leu Thr Leu Ser Ser Ala Met Trp Phe	
450 455 460	
TCC TGG GGC GTC CTG CTC AAC TCC GGC ATC GGG GAA GGC GCC CCC AGA	1440
Ser Trp Gly Val Leu Leu Asn Ser Gly Ile Gly Glu Gly Ala Pro Arg	
465 470 475 480	
AGC TTC TCA GCG CGC ATC CTG GGC ATG GTG TGG GCC GGC TTT GCC ATG	1488
Ser Phe Ser Ala Arg Ile Leu Gly Met Val Trp Ala Gly Phe Ala Met	
485 490 495	
ATC ATC GTG GCC TCC TAC ACC GGC AAC CTG GCG GCC TTC CTG GTG CTC	1536
Ile Ile Val Ala Ser Tyr Thr Ala Asn Leu Ala Ala Phe Leu Val Leu	
500 505 510	
GAC CGG CGG GAG GAG CGC ATC ACG GGC ATC AAC GAC CCT CGG CTG AGG	1584
Asp Arg Pro Glu Glu Arg Ile Thr Gly Ile Asn Asp Pro Arg Leu Arg	
515 520 525	
AAC CCC TCG GAC AAG TTT ATC TAC GCC ACG GTG AAG CAG AGC TCC GTG	1632
Asn Pro Ser Asp Lys Phe Ile Tyr Ala Thr Val Lys Gln Ser Ser Val	
530 535 540	
GAT ATC TAC TTC CGG CGC CAG GTG GAG CTG AGC ACC ATG TAC CGG CAT	1680
Asp Ile Tyr Phe Arg Arg Gln Val Glu Leu Ser Thr Met Tyr Arg His	
545 550 555 560	

ATG GAG AAG CAC AAC TAC GAG AGT GCG GCG GAG GCC ATC CAG GCC GTG Met Glu Lys His Asn Tyr Glu Ser Ala Ala Glu Ala Ile Gln Ala Val 565 570 575	1728
AGA GAC AAC AAG CTG CAT GCC TTC ATC TGG GAC TCG GCG GTG CTG GAG Arg Asp Asn Lys Leu His Ala Phe Ile Trp Asp Ser Ala Val Leu Glu 580 585 590	1776
TTC GAG GCC TCG CAG AAG TGC GAC CTG GTG ACG ACT GGA GAG CTG TTT Phe Glu Ala Ser Gln Lys Cys Asp Leu Val Thr Thr Gly Glu Leu Phe 595 600 605	1824
TTC CGC TCG GGC TTC GGC ATA GGC ATG CGC AAA GAC AGC CCC TGG AAG Phe Arg Ser Gly Phe Gly Ile Gly Met Arg Lys Asp Ser Pro Trp Lys 610 615 620	1872
CAG AAC GTC TCC CTG TCC ATC CTC AAG TCC CAC GAG AAT GGC TTC ATG Gln Asn Val Ser Leu Ser Ile Leu Lys Ser His Glu Asn Gly Phe Met 625 630 635 640	1920
GAA GAC CTG GAC AAG ACG TGG GTT CGG TAT CAG GAA TGT GAC TCG CGC Glu Asp Leu Asp Lys Thr Trp Val Arg Tyr Gln Glu Cys Asp Ser Arg 645 650 655	1968
AGC AAC GCC CCT GCG ACC CTT ACT TTT GAG AAC ATG GCC GGG GTC TTC Ser Asn Ala Pro Ala Thr Leu Thr Phe Glu Asn Met Ala Gly Val Phe 660 665 670	2016
ATG CTG GTA GCT GGG GGC ATC GTG GCC GGG ATC TTC CTG ATT TTC ATC Met Leu Val Ala Gly Gly Ile Val Ala Gly Ile Phe Leu Ile Phe Ile 675 680 685	2064
GAG ATT GCC TAC AAG CGG CAC AAG GAT GCT CGC CGG AAG CAG ATG CAG Glu Ile Ala Tyr Lys Arg His Lys Asp Ala Arg Arg Lys Gln Met Gln 690 695 700	2112
CTG GCC TTT GCC GCC GTT AAC GTG TGG CGG AAG AAC CTG CAG GAT AGA Leu Ala Phe Ala Ala Val Asn Val Trp Arg Lys Asn Leu Gln Asp Arg 705 710 715 720	2160
AAG AGT GGT AGA GCA GAG CCT GAC CCT AAA AAG AAA GCC ACA TTT AGG Lys Ser Gly Arg Ala Glu Pro Asp Pro Lys Lys Ala Thr Phe Arg 725 730 735	2208
GCT ATC ACC ACC CTG GCT TCC AGC TTC AAG AGG CGT AGG TCC TCC Ala Ile Thr Ser Thr Leu Ala Ser Ser Phe Lys Arg Arg Arg Ser Ser 740 745 750	2256
AAA GAC ACG CAG TAC CAT CCC ACT GAT ATC ACG GGC CGG CTC AAC CTC Lys Asp Thr Gln Tyr His Pro Thr Asp Ile Thr Gly Pro Leu Asn Leu 755 760 765	2304
TCA GAT CCC TCG GTC AGC ACC GTG GTG TGAGGGCCCCC GGAGGGCGCCC Ser Asp Pro Ser Val Ser Thr Val Val 770 775	2351
ACCTGCCAG TTAGCCCCGGC CAAGGACACT GATGGGTCT GCTGCTGGG AAGGCCTGAG	2411
GGAAAGTCCAC CGGCCCCAGA GACTGCCAC CCTGGGCCTC CGGTCCGTCC GCGCGCCAC	2471
CCCCTGCCT GCGGGCAGC CCCTGCTGGA CCAAGGTGCG GACCGGAGCG GCTGAGGACG	2531
GGGCAGAGC	2540

'i SEQUENCE CHARACTERISTICS:
(A) LENGTH: 777 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NC:16:

Asn Asp His Phe Thr Pro Thr Pro Val Ser Tyr Thr Ala Gly Phe Tyr
1 5 10 15

Arg Ile Pro Val Leu Gly Leu Thr Thr Arg Met Ser Ile Tyr Ser Asp
20 25 30

Lys Ser Ile His Leu Ser Phe Leu Arg Thr Val Pro Pro Tyr Ser His
35 40 45

Gln Ser Ser Val Trp Phe Glu Met Met Arg Val Tyr Ser Trp Asn His
50 55 60

Ile Ile Leu Leu Val Ser Asp Asp His Glu Gly Arg Ala Ala Gln Lys
65 70 75 80

Arg Leu Glu Thr Leu Leu Glu Glu Arg Glu Ser Lys Ser Lys Lys Arg
85 90 95

Asn Tyr Glu Asn Leu Asp Gln Leu Ser Tyr Asp Asn Lys Arg Gly Pro
100 105 110

Lys Ala Glu Lys Val Leu Gln Phe Asp Pro Gly Thr Lys Asn Val Thr
115 120 125

Ala Leu Leu Met Glu Ala Lys Glu Leu Glu Ala Arg Val Ile Ile Leu
130 135 140

Ser Ala Ser Glu Asp Asp Ala Ala Thr Val Tyr Arg Ala Ala Ala Met
145 150 155 160

Leu Asn Met Thr Gly Asn Thr Asn Ile Trp Lys Thr Gly Pro Leu Phe
165 170 175

Lys Arg Val Leu Met Ser Ser Lys Tyr Ala Asp Gly Val Thr Gly Arg
180 185 190

Val Glu Phe Asn Glu Asp Gly Asp Arg Lys Phe Ala Asn Tyr Ser Ile
195 200 205

Met Asn Leu Gln Asn Arg Lys Leu Val Gln Val Gly Ile Tyr Asn Gly
210 215 220

Thr His Val Ile Pro Asn Asp Arg Lys Ile Ile Trp Pro Gly Gly Glu
225 230 235 240

Thr Glu Lys Pro Arg Gly Tyr Gln Met Ser Thr Arg Leu Lys Ile Val
245 250 255

Thr Ile His Gln Glu Pro Phe Val Tyr Val Lys Pro Thr Leu Ser Asp
260 265 270

Gly Thr Cys Lys Glu Glu Phe Thr Val Asn Gly Asp Pro Val Lys Lys
275 280 285

Val Ile Cys Thr Gly Pro Asn Asp Thr Ser Pro Gly Ser Pro Arg His
290 295 300

Thr Val Pro Gln Cys Cys Tyr Gly Phe Cys Ile Asp Leu Leu Ile Lys

305 310 315 320
Leu Ala Arg Thr Met Asn Phe Thr Tyr Glu Val His Leu Val Ala Asp
 325 330 335
Gly Lys Phe Gly Thr Gln Glu Arg Val Asn Asn Ser Asn Lys Lys Glu
 340 345 350
Trp Asn Gly Met Met Gly Glu Leu Leu Ser Gly Gln Ala Asp Met Ile
 355 360 365

Val Ala Pro Leu Thr Ile Asn Asn Glu Arg Ala Gln Tyr Ile Glu Phe
 370 375 380
Ser Lys Pro Phe Lys Tyr Gln Gly Leu Thr Ile Leu Val Lys Lys Glu
 385 390 395 400
Ile Pro Arg Ser Thr Leu Asp Ser Phe Met Gln Pro Phe Gln Ser Thr
 405 410 415
Leu Trp Leu Leu Val Gly Leu Ser Val His Val Val Ala Val Met Leu
 420 425 430
Tyr Leu Leu Asp Arg Phe Ser Pro Phe Gly Arg Phe Lys Val Asn Ser
 435 440 445
Glu Glu Glu Glu Asp Ala Leu Thr Leu Ser Ser Ala Met Trp Phe
 450 455 460
Ser Trp Gly Val Leu Leu Asn Ser Gly Ile Gly Glu Gly Ala Pro Arg
 465 470 475 480
Ser Phe Ser Ala Arg Ile Leu Gly Met Val Trp Ala Gly Phe Ala Met
 485 490 495
Ile Ile Val Ala Ser Tyr Thr Ala Asn Leu Ala Ala Phe Leu Val Leu
 500 505 510
Asp Arg Pro Glu Glu Arg Ile Thr Gly Ile Asn Asp Pro Arg Leu Arg
 515 520 525
Asn Pro Ser Asp Lys Phe Ile Tyr Ala Thr Val Lys Gln Ser Ser Val
 530 535 540
Asp Ile Tyr Phe Arg Arg Gln Val Glu Leu Ser Thr Met Tyr Arg His
 545 550 555 560
Met Glu Lys His Asn Tyr Glu Ser Ala Ala Glu Ala Ile Gln Ala Val
 565 570 575
Arg Asp Asn Lys Leu His Ala Phe Ile Trp Asp Ser Ala Val Leu Glu
 580 585 590
Phe Glu Ala Ser Gln Lys Cys Asp Leu Val Thr Thr Gly Glu Leu Phe
 595 600 605
Phe Arg Ser Gly Phe Gly Ile Gly Met Arg Lys Asp Ser Pro Trp Lys
 610 615 620
Gln Asn Val Ser Leu Ser Ile Leu Lys Ser His Glu Asn Gly Phe Met
 625 630 635 640
Glu Asp Leu Asp Lys Thr Trp Val Arg Tyr Gln Glu Cys Asp Ser Arg
 645 650 655
Ser Asn Ala Pro Ala Thr Leu Thr Phe Glu Asn Met Ala Gly Val Phe

660

665

670

Met Leu Val Ala Gly Gly Ile Val Ala Gly Ile Phe Leu Ile Phe Ile
675 680 685

Glu Ile Ala Tyr Lys Arg His Lys Asp Ala Arg Arg Lys Gln Met Gln
690 695 700

Leu Ala Phe Ala Ala Val Asn Val Trp Arg Lys Asn Leu Gln Asp Arg
705 710 715 720

Lys Ser Gly Arg Ala Glu Pro Asp Pro Lys Lys Lys Ala Thr Phe Arg
725 730 735

Ala Ile Thr Ser Thr Leu Ala Ser Ser Phe Lys Arg Arg Arg Ser Ser
740 745 750

Lys Asp Thr Gln Tyr His Pro Thr Asp Ile Thr Gly Pro Leu Asn Leu
755 760 765

Ser Asp Pro Ser Val Ser Thr Val Val
770 775

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 595 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..576

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GAA GAC CTG GAC AAG ACG TGG GTT CGG TAT CAG GAA TGT GAC TCG CGC 48
Glu Asp Leu Asp Lys Thr Trp Val Arg Tyr Gln Glu Cys Asp Ser Arg
1 5 10 15

AGC AAC GCC CCT GCG ACC CTT ACT TTT GAG AAC ATG GCC GGG GTC TTC 96
Ser Asn Ala Pro Ala Thr Leu Thr Phe Glu Asn Met Ala Gly Val Phe
20 25 30

ATG CTG GTA GCT GGG GGC ATC GTG GCC GGG ATC TTC CTG ATT TTC ATC 144
Met Leu Val Ala Gly Ile Val Ala Gly Ile Phe Leu Ile Phe Ile
35 40 45

GAG ATT GCC TAC AAG CGG CAC AAG GAT GCT CGC CGG AAG CAG ATG CAG 192
Glu Ile Ala Tyr Lys Arg His Lys Asp Ala Arg Arg Lys Gln Met Gln
50 55 60

CTG GCC TTT GCC GCC GTT AAC GTG TGG CGG AAG AAC CTG CAG GAT AGA 240
Leu Ala Phe Ala Ala Val Asn Val Trp Arg Lys Asn Leu Gln Asp Arg
65 70 75 80

AAG AGT GGT AGA GCA GAG CCT GAC CCT AAA AAG AAA GCC ACA TTT AGG 288
Lys Ser Gly Arg Ala Glu Pro Asp Pro Lys Lys Lys Ala Thr Phe Arg
85 90 95

GCT ATC ACC TCC ACC CTG GCT TCC AGC TTC AAG AGG CGT AGG TCC TCC Ala Ile Thr Ser Thr Leu Ala Ser Ser Phe Lys Arg Arg Arg Ser Ser 100 105 110	336
AAA GAC ACG CTG GCT CCG GAC TGT CTT CAA CCC TGC CCT GCA CCT TGG Lys Asp Thr Leu Ala Arg Asp Cys Leu Gln Pro Cys Pro Ala Pro Trp 115 120 125	384
GCA CGG GAG AGC GCC ACC CGC CCG CCC CCG CCC TCG CTC CGG GTG CGT Ala Arg Glu Ser Ala Thr Arg Pro Pro Pro Ser Leu Arg Val Arg 130 135 140	432
GAC CGG CCC GCC ACC TTG TAC AGA ACC AGC ACT CCC AGG GCC CGA GCG Asp Arg Pro Ala Thr Leu Tyr Arg Thr Ser Thr Pro Arg Ala Arg Ala 145 150 155 160	480
CGT GCC TTC CCC GTG CGC AGC CGC GCT CTG CCC CTC CGT CCC CAG GGT Arg Ala Phe Pro Val Arg Ser Arg Ala Leu Pro Leu Arg Pro Gln Gly 165 170 175	528
GCA GGC GCG CAC CGC CCA ACC CCC ACC TCC CGG TGT ATG CAG TGG TGATGCCTAA Ala Gly Ala His Arg Pro Thr Pro Thr Ser Arg Cys Met Gln Trp 180 185 190	583
AGGAATGTCA CG	595

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 191 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Glu Asp Leu Asp Lys Thr Trp Val Arg Tyr Gln Glu Cys Asp Ser Arg 1 5 10 15
Ser Asn Ala Pro Ala Thr Leu Thr Phe Glu Asn Met Ala Gly Val Phe 20 25 30
Met Leu Val Ala Gly Gly Ile Val Ala Gly Ile Phe Leu Ile Phe Ile 35 40 45
Glu Ile Ala Tyr Lys Arg His Lys Asp Ala Arg Arg Lys Gln Met Gln 50 55 60
Leu Ala Phe Ala Ala Val Asn Val Trp Arg Lys Asn Leu Gln Asp Arg 65 70 75 80
Lys Ser Gly Arg Ala Glu Pro Asp Pro Lys Lys Lys Ala Thr Phe Arg 85 90 95
Ala Ile Thr Ser Thr Leu Ala Ser Ser Phe Lys Arg Arg Ser Ser 100 105 110
Lys Asp Thr Leu Ala Arg Asp Cys Leu Gln Pro Cys Pro Ala Pro Trp 115 120 125
Ala Arg Glu Ser Ala Thr Arg Pro Pro Pro Ser Leu Arg Val Arg 130 135 140
Asp Arg Pro Ala Thr Leu Tyr Arg Thr Ser Thr Pro Arg Ala Arg Ala 145 150 155 160

Arg Ala Phe Pro Val Arg Ser Arg Ala Leu Pro Leu Arg Pro Gln Gly
165 171 175

Ala Gly Ala His Arg Pro Thr Pro Tyr Ser Arg Cys Met Gln Trp
180 185 190

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3935 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 262..3030

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CAAGCCGGGC GTTCGGAGCT GTGCCCGGCC CGCTTCAGC ACCGCGGACA GCGCCGGCCG	60
CGTGGGGCTG AGCGCCGAGC CCCC3CGCAC GCTTCAGCCC CCCTTCCTC GGCGACGTC	120
CCGGGACCGC CGCTCCGGGG GAGACGTGGC GTCCGCAGCC CGCGGGGCCG GGCGAGCGCA	180
GGACGGCCCG GAAGCCCCGC GGGGGATGCG CCGAGGGCCC CGCGTTCGCG CCGCGCAGAG	240
CCAGGCCCCGC GGCCCGAGCC C ATG AGC ACC ATG CGC CTG CTG ACG CTC GCC	291
Met Ser Thr Met Arg Leu Leu Thr Leu Ala	
1 5 10	
CTG CTG TTC TCC TGC TCC GTC CST GCC GCG TGC GAC CCC AAG ATC	339
Leu Leu Phe Ser Cys Ser Val Ala Arg Ala Ala Cys Asp Pro Lys Ile	
15 20 25	
GTC AAC ATT GGC GCG GTG CTG AGC ACG CGG AAG CAC GAG CAG ATG TTC	387
Val Asn Ile Gly Ala Val Leu Ser Thr Arg Lys His Glu Gln Met Phe	
30 35 40	
CGC GAG GCC GTG AAC CAG GCC AAC AAG CGG CAC GGC TCC TGG AAG ATT	435
Arg Glu Ala Val Asn Gln Ala Asn Lys Arg His Gly Ser Trp Lys Ile	
45 50 55	
CAG CTC AAT GCC ACC TCC GTC ACG CAC AAG CCC AAC GCC ATC CAG ATG	483
Gln Leu Asn Ala Thr Ser Val Thr His Lys Pro Asn Ala Ile Gln Met	
60 65 70	
GCT CTG TCG GTG TGC GAG GAC CTC ATC TCC AGC CAG GTC TAC GCC ATC	531
Ala Leu Ser Val Cys Glu Asp Leu Ile Ser Ser Gln Val Tyr Ala Ile	
75 80 85 90	
CTA GTT AGC CAT CCA CCT ACC CCC AAC GAC CAC TTC ACT CCC ACC CCT	579
Leu Val Ser His Pro Pro Thr Pro Asn Asp His Phe Thr Pro Thr Pro	
95 100 105	
GTC TCC TAC ACA GCC GGC TTC TAC CGC ATA CCC GTG CTG GGG CTG ACC	627
Val Ser Tyr Thr Ala Gly Phe Tyr Arg Ile Pro Val Leu Gly Leu Thr	
110 115 120	
ACC CGC ATG TCC ATC TAC TCG GAC AAG AGC ATC CAC CTG AGC TTC CTG	675
Thr Arg Met Ser Ile Tyr Ser Asp Lys Ser Ile His Leu Ser Phe Leu	

125

130

135

CGC ACC GTG CCG CCC TAC TCC CAC CAG TCC AGC GTG TGG TTT GAG ATG Arg Thr Val Pro Pro Tyr Ser His Gln Ser Ser Val Trp Phe Glu Met 140	145	150	723
ATG CGT GTC TAC AGC TGG AAC CAC ATC ATC CTG CTG GTC AGC GAC GAC Met Arg Val Tyr Ser Trp Asn His Ile Ile Leu Leu Val Ser Asp Asp 155	160	165	771
CAC GAG GGC CGG GCG GCT CAG AAA CGC CTG GAG ACG CTG CTG GAG GAG His Glu Gly Arg Ala Ala Gln Lys Arg Leu Glu Thr Leu Leu Glu Glu 175	180	185	819
CGT GAG TCC AAG GCA GAG AAG GTG CTG CAG TTT GAC CCA GGG ACC AAG Arg Glu Ser Lys Ala Glu Lys Val Leu Gln Phe Asp Pro Gly Thr Lys 190	195	200	867
AAC GTG ACG GCC CTG CTG ATG GAG GCG AAA GAG CTG GAG GCC CGG GTC Asn Val Thr Ala Leu Leu Met Glu Ala Lys Glu Leu Glu Ala Arg Val 205	210	215	915
ATC ATC CTT TCT GCC AGC GAG GAC GAT GCT GCC ACT GTA TAC CGC GCA Ile Ile Leu Ser Ala Ser Glu Asp Asp Ala Ala Thr Val Tyr Arg Ala 220	225	230	963
GCC GCG ATG CTG AAC ATG ACG GGC TCC GGG TAC GTG TGG CTG GTC GGC Ala Ala Met Leu Asn Met Thr Gly Ser Gly Tyr Val Trp Leu Val Gly 235	240	245	1011
GAG CGC GAG ATC TCG GGG AAC GCC CTG CGC TAC GCC CCA GAC GGC ATC Glu Arg Glu Ile Ser Gly Asn Ala Leu Arg Tyr Ala Pro Asp Gly Ile 255	260	265	1059
CTC GGG CTG CAG CTC ATC AAC GGC AAG AAC GAG TCG GCC CAC ATC AGC Leu Gly Leu Gln Leu Ile Asn Gly Lys Asn Glu Ser Ala His Ile Ser 270	275	280	1107
GAC GCC GTG GGC GTG GTG GCC CAG GCC GTG CAC GAG CTC CTC GAG AAG Asp Ala Val Gly Val Val Ala Gln Ala Val His Glu Leu Leu Glu Lys 285	290	295	1155
GAG AAC ATC ACC GAC CCG CCG CGG GGC TGC GTG GGC AAC ACC AAC ATC Glu Asn Ile Thr Asp Pro Pro Arg Gly Cys Val Gly Asn Thr Asn Ile 300	305	310	1203
TGG AAG ACC GGG CCG CTC TTC AAG AGA GTG CTG ATG TCT TCC AAG TAT Trp Lys Thr Gly Pro Leu Phe Lys Arg Val Leu Met Ser Ser Lys Tyr 315	320	325	1251
GCG GAT GGG GTG ACT GGT CGC GTG GAG TTC AAT GAG GAT GGG GAC CGG Ala Asp Gly Val Thr Gly Arg Val Glu Phe Asn Glu Asp Gly Asp Arg 335	340	345	1299
AAG TTC GCC AAC TAC AGC ATC ATG AAC CTG CAG AAC CGC AAG CTG GTG Lys Phe Ala Asn Tyr Ser Ile Met Asn Leu Gln Asn Arg Lys Leu Val 350	355	360	1347
CAA GTG GGC ATC TAC AAT GGC ACC CAC GTC ATC CCT AAT GAC AGG AAG Gln Val Gly Ile Tyr Asn Gly Thr His Val Ile Pro Asn Asp Arg Lys 365	370	375	1395
ATC ATC TGG CCA GGC GGA GAG ACA GAG AAG CCT CGA GGG TAC CAG ATG Ile Ile Trp Pro Gly Gly Glu Thr Glu Lys Pro Arg Gly Tyr Gln Met 380	385	390	1443

TCC ACC AGA CTG AAG ATT GTG ACG ATC CAC CAG GAG CCC TTC GTG TAC	1491
Ser Thr Arg Leu Lys Ile Val Thr Ile His Gln Glu Pro Phe Val Tyr	
395 400 405 410	
GTC AAG CCC ACG CTG AGT GAT GGG ACA TGC AAG GAG GAG TTC ACA GTC	1539
Val Lys Pro Thr Leu Ser Asp Gly Thr Cys Lys Glu Glu Phe Thr Val	
415 420 425	
AAC GGC GAC CCA GTC AAG AAG GTG ATC TGC ACC GGG CCC AAC GAC ACG	1587
Asn Gly Asp Pro Val Lys Lys Val Ile Cys Thr Gly Pro Asn Asp Thr	
430 435 440	
TCG CCG GGC AGC CCC CGC CAC ACG GTG CCT CAG TGT TGC TAC GGC TTT	1635
Ser Pro Gly Ser Pro Arg His Thr Val Pro Gln Cys Cys Tyr Gly Phe	
445 450 455	
TGC ATC GAC CTG CTC ATC AAG CTG GCA CGG ACC ATG AAC TTC ACC TAC	1683
Cys Ile Asp Leu Leu Ile Lys Leu Ala Arg Thr Met Asn Phe Thr Tyr	
460 465 470	
GAG GTG CAC CTG GTG GCA GAT GGC AAG TTC GGC ACA CAG GAG CGG GTG	1731
Glu Val His Leu Val Ala Asp Gly Lys Phe Gly Thr Gln Glu Arg Val	
475 480 485 490	
AAC AAC AGC AAC AAG AAG GAG TGG AAT GGG ATG ATG GGC GAG CTG CTC	1779
Asn Asn Ser Asn Lys Lys Glu Trp Asn Gly Met Met Gly Glu Leu Leu	
495 500 505	
AGC GGG CAG GCA GAC ATG ATC GTG GCG CCG CTA ACC ATA AAC AAC GAG	1827
Ser Gly Gln Ala Asp Met Ile Val Ala Pro Leu Thr Ile Asn Asn Glu	
510 515 520	
CGC GCG CAG TAC ATC GAG TTT TCC AAG CCC TTC AAG TAC CAG GGC CTG	1875
Arg Ala Gln Tyr Ile Glu Phe Ser Lys Pro Phe Lys Tyr Gln Gly Leu	
525 530 535	
ACT ATT CTG GTC AAG AAG GAG ATT CCC CGG AGC ACG CTG GAC TCG TTC	1923
Thr Ile Leu Val Lys Lys Glu Ile Pro Arg Ser Thr Leu Asp Ser Phe	
540 545 550	
ATG CAG CCG TTC CAG AGC ACA CTG TGG CTG CTG GTG GGG CTG TCG GTG	1971
Met Gln Pro Phe Gln Ser Thr Leu Trp Leu Leu Val Gly Leu Ser Val	
555 560 565 570	
CAC GTG GTG GCC GTG ATG CTG TAC CTG CTG GAC CGC TTC AGC CCC TTC	2019
His Val Val Ala Val Met Leu Tyr Leu Leu Asp Arg Phe Ser Pro Phe	
575 580 585	
GCG CGG TTC AAG GTG AAC AGC GAG GAG GAG GAG GAC GCA CTG ACC	2067
Gly Arg Phe Lys Val Asn Ser Glu Glu Glu Glu Asp Ala Leu Thr	
590 595 600	
CTG TCC TCG GCC ATG TGG TTC TCC TGG GGC GTC CTG CTC AAC TCC GGC	2115
Leu Ser Ser Ala Met Trp Phe Ser Trp Gly Val Leu Leu Asn Ser Gly	
605 610 615	
ATC GGG GAA GGC GCC CCC AGA AGC TTC TCA GCG CGC ATC CTG GGC ATG	2163
Ile Gly Glu Gly Ala Pro Arg Ser Phe Ser Ala Arg Ile Leu Gly Met	
620 625 630	
GTG TGG GCC GGC TTT GCC ATG ATC ATC GTG GCC TCC TAC ACC GCC AAC	2211
Val Trp Ala Gly Phe Ala Met Ile Ile Val Ala Ser Tyr Thr Ala Asn	
635 640 645 650	
CTG GCG GCC TTC CTG GTG CTG GAC CGG CCG GAG GAG CGC ATC ACG GGC	2259
Leu Ala Ala Phe Leu Val Leu Asp Arg Pro Glu Glu Arg Ile Thr Gly	
655 660 665	

ATC AAC GAC CCT CGG CTG AGG AAC CCC TCG GAC AAG TTT ATC TAC GCC Ile Asn Asp Pro Arg Leu Arg Asn Pro Ser Asp Lys Phe Ile Tyr Ala 670 675 680	2307
ACG GTG AAG CAG AGC TCC GTG GAT ATC TAC TTC CGG CGC CAG GTG GAG Thr Val Lys Gln Ser Ser Val Asp Ile Tyr Phe Arg Arg Gln Val Glu 685 690 695	2355
CTG AGC ACC ATG TAC CGG CAT ATG GAG AAG CAC AAC TAC GAG AGT GCG Leu Ser Thr Met Tyr Arg His Met Glu Lys His Asn Tyr Glu Ser Ala 700 705 710	2403
GCG GAG GCC ATC CAG GCC GTG AGA GAC AAC AAG CTG CAT GCC TTC ATC Ala Glu Ala Ile Gln Ala Val Arg Asp Asn Lys Leu His Ala Phe Ile 715 720 725 730	2451
TGG GAC TCG GCG GTG CTG GAG TTC GAG GCC TCG CAG AAG TGC GAC CTG Trp Asp Ser Ala Val Leu Glu Phe Glu Ala Ser Gln Lys Cys Asp Leu 735 740 745	2499
GTG ACG ACT GGA GAG CTG TTT TTC CGC TCG GGC TTC GGC ATA GGC ATG Val Thr Gly Glu Leu Phe Phe Arg Ser Gly Phe Gly Ile Gly Met 750 755 760	2547
CGC AAA GAC AGC CCC TGG AAG CAG AAC GTC TCC CTG TCC ATC CTC AAG Arg Lys Asp Ser Pro Trp Lys Gln Asn Val Ser Leu Ser Ile Leu Lys 765 770 775	2595
TCC CAC GAG AAT GGC TTC ATG GAA GAC CTG GAC AAG ACG TGG GTT CGG Ser His Glu Asn Gly Phe Met Glu Asp Leu Asp Lys Thr Trp Val Arg 780 785 790	2643
TAT CAG GAA TGT GAC TCG CGC AGC AAC GCC CCT GCG ACC CTT ACT TTT Tyr Gln Glu Cys Asp Ser Arg Ser Asn Ala Pro Ala Thr Leu Thr Phe 795 800 805 810	2691
GAG AAC ATG GCC GGG GTC TTC ATG CTG GTA GCT GGG GGC ATC GTG GCC Glu Asn Met Ala Gly Val Phe Met Leu Val Ala Gly Gly Ile Val Ala 815 820 825	2739
GGG ATC TTC CTG ATT TTC ATC GAG ATT GCC TAC AAG CGG CAC AAG GAT Gly Ile Phe Leu Ile Phe Ile Glu Ile Ala Tyr Lys Arg His Lys Asp 830 835 840	2787
GCT CGC CGG AAG CAG ATG CAG CTG GCC TTT GCC GCC GTT AAC GTG TGG Ala Arg Arg Lys Gln Met Gln Leu Ala Phe Ala Ala Val Asn Val Trp 845 850 855	2835
CGG AAG AAC CTG CAG GAT AGA AAG AGT GGT AGA GCA GAG CCT GAC CCT Arg Lys Asn Leu Gln Asp Arg Lys Ser Gly Arg Ala Glu Pro Asp Pro 860 865 870	2883
AAA AAG AAA GCC ACA TTT AGG GCT ATC ACC TCC ACC CTG GCT TCC AGC Lys Lys Ala Thr Phe Arg Ala Ile Thr Ser Thr Leu Ala Ser Ser 875 880 885 890	2931
TTC AAG AGG CGT AGG TCC TCC AAA GAC ACG CAG TAC CAT CCC ACT GAT Phe Lys Arg Arg Ser Ser Lys Asp Thr Gln Tyr His Pro Thr Asp 895 900 905	2979
ATC ACG GGC CCG CTC AAC CTC TCA GAT CCC TCG GTC AGC ACC GTG GTG Ile Thr Gly Pro Leu Asn Leu Ser Asp Pro Ser Val Ser Thr Val Val 910 915 920	3027
TGAGGCCCGGGGGAGGGCGCCCC ACCTGCCAG TTAGCCCCGGC CAAGGGACACT GATGGGTCT GCTGCTCGGG AAGGCCCTGAG GGAAGCCCAC CGGCCCCAGA GACTGCCAC CCTGGGCCCTC	3087
	3147

CCGTCCGTCC	GCCCCCCCAC	CCCCTGCCT	GGCGGGCAGC	CCCTGTTGGA	CCAAGGTGCG	3207
GACCGGAGCG	GCTGAGGACG	GGGCAGAGCT	GAGTCGGCTG	GGCAGGGCCG	CAGGGCGCTC	3267
CGGCAGAGGC	AGGCCCTGG	GGTCTCTGAG	CAGTGGGGAG	CGGGGGCTAA	CTGCCCCCAG	3327
GCGGAGGGC	TTGGAGCAGA	GACGGCAGCC	CCATCCTTCC	CGCAGJACCA	GCCTGAGCCA	3387
CAGTGGGCC	CATGGCCCCA	GCTGGCTGGG	TCGCCCCCTCC	TCGGCGCCT	GCGCTCCTCT	3447
GCAGCCTGAG	CTCCACCCCTC	CCCTCTTCTT	CGGGCACCGC	CCACCAAACA	CCCCGTCTGC	3507
CCCTTGACGC	CACACGCCGG	GGCTGGCGCT	GCCCTCCCCC	ACGGCCGTCC	CTGACTTCCC	3567
AGCTGGCAGC	GCCTCCCGCC	GCCTCGGGCC	GCCTCCTCCA	GAATCGAGAG	GGCTGAGCCC	3627
CTCCTCTCCT	CGTCCGGCCT	GCAGCACAGA	AGGGGGCCTC	CCCGGGGTC	CCCGGACGCT	3687
GGCTCGGGAC	TGTCTTCAAC	CCTGCCCTGC	ACCTTGGGCA	CGGGAGAGCG	CCACCCGCC	3747
GCCCCCGCCC	TCGCTCCGGG	TGCGTGACCG	GCCCCGCCACC	TTGTACAGAA	CCAGCACTCC	3807
CAGGGCCCGA	GCGCGTGCCT	TCCCCGTGCG	CAGCCGCGCT	CTGCCCCCTCC	GTCCCCAGGG	3867
TGCAGGGCGCG	CACCGCCCAA	CCCCCACCTC	CCGGTGTATG	CAGTGGTGAT	GCCTAAAGGA	3927
ATGTCACG						3935

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 922 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Met	Ser	Thr	Met	Arg	Leu	Leu	Thr	Leu	Ala	Leu	Leu	Phe	Ser	Cys	Ser
1				5				10						15	
Val	Ala	Arg	Ala	Ala	Cys	Asp	Pro	Lys	Ile	Val	Asn	Ile	Gly	Ala	Val
				20				25				30			
Leu	Ser	Thr	Arg	Lys	His	Glu	Gln	Met	Phe	Arg	Glu	Ala	Val	Asn	Gln
				35			40				45				
Ala	Asn	Lys	Arg	His	Gly	Ser	Trp	Lys	Ile	Gln	Leu	Asn	Ala	Thr	Ser
				50			55				60				
Val	Thr	His	Lys	Pro	Asn	Ala	Ile	Gln	Met	Ala	Leu	Ser	Val	Cys	Glu
				65			70				75		80		
Asp	Leu	Ile	Ser	Ser	Gln	Val	Tyr	Ala	Ile	Leu	Val	Ser	His	Pro	Pro
				85			90				95				
Thr	Pro	Asn	Asp	His	Phe	Thr	Pro	Thr	Pro	Val	Ser	Tyr	Thr	Ala	Gly
				100			105				110				
Phe	Tyr	Arg	Ile	Pro	Val	Leu	Gly	Leu	Thr	Thr	Arg	Met	Ser	Ile	Tyr
				115			120				125				
Ser	Asp	Lys	Ser	Ile	His	Leu	Ser	Phe	Leu	Arg	Thr	Val	Pro	Pro	Tyr
				130			135				140				

Ser His Gln Ser Ser Val Trp Phe Glu Met Met Arg Asn Tyr Ser Trp
145 150 155 160

Asn His Ile Ile Leu Leu Val Ser Asp Asp His Glu Gln Arg Ala Ala
165 170 175

Gln Lys Arg Leu Glu Thr Leu Leu Glu Glu Arg Gln Ser Lys Ala Glu
180 185 190

Lys Val Leu Gln Phe Asp Pro Gly Thr Lys Asn Val Thr Ala Leu Leu
195 200 205

Met Glu Ala Lys Glu Leu Glu Ala Arg Val Ile Ile Leu Ser Ala Ser
210 215 220

Glu Asp Asp Ala Ala Thr Val Tyr Arg Ala Ala Met Leu Asn Met
225 230 235 240

Thr Gly Ser Gly Tyr Val Trp Leu Val Gly Glu Arg Glu Ile Ser Gly
245 250 255

Asn Ala Leu Arg Tyr Ala Pro Asp Gly Ile Leu Gly Leu Gln Leu Ile
260 265 270

Asn Gly Lys Asn Glu Ser Ala His Ile Ser Asp Ala Val Gly Val Val
275 280 285

Ala Gln Ala Val His Glu Leu Leu Glu Lys Glu Asn Ile Thr Asp Pro
290 295 300

Pro Arg Gly Cys Val Gly Asn Thr Asn Ile Trp Lys Thr Gly Pro Leu
305 310 315 320

Phe Lys Arg Val Leu Met Ser Ser Lys Tyr Ala Asp Gly Val Thr Gly
325 330 335

Arg Val Glu Phe Asn Glu Asp Gly Asp Arg Lys Phe Ala Asn Tyr Ser
340 345 350

Ile Met Asn Leu Gln Asn Arg Lys Leu Val Gln Val Gly Ile Tyr Asn
355 360 365

Gly Thr His Val Ile Pro Asn Asp Arg Lys Ile Ile Trp Pro Gly Gly
370 375 380

Glu Thr Glu Lys Pro Arg Gly Tyr Gln Met Ser Thr Arg Leu Lys Ile
385 390 395 400

Val Thr Ile His Gln Glu Pro Phe Val Tyr Val Lys Pro Thr Leu Ser
405 410 415

Asp Gly Thr Cys Lys Glu Glu Phe Thr Val Asn Gly Asp Pro Val Lys
420 425 430

Lys Val Ile Cys Thr Gly Pro Asn Asp Thr Ser Pro Gly Ser Pro Arg
435 440 445

His Thr Val Pro Gln Cys Cys Tyr Gly Phe Cys Ile Asp Leu Leu Ile
450 455 460

Lys Leu Ala Arg Thr Met Asn Phe Thr Tyr Glu Val His Leu Val Ala
465 470 475 480

Asp Gly Lys Phe Gly Thr Gln Glu Arg Val Asn Asn Ser Asn Lys Lys
485 490 495

Glu Trp Asn Gly Met Met Gly Glu Leu Leu Ser Gly Gln Ala Asp Met

500 505 510
Ile Val Ala Pro Leu Thr Ile Asn Asn Glu Arg Ala Gln Tyr Ile Glu
515 520 525
Phe Ser Lys Pro Phe Lys Tyr Gln Gly Leu Thr Ile Leu Val Lys Lys
530 535 540

Glu Ile Pro Arg Ser Thr Leu Asp Ser Phe Met Gln Pro Phe Gln Ser
545 550 555 560
Thr Leu Trp Leu Leu Val Gly Leu Ser Val His Val Val Ala Val Met
565 570 575
Leu Tyr Leu Leu Asp Arg Phe Ser Pro Phe Gly Arg Phe Lys Val Asn
580 585 590
Ser Glu Glu Glu Glu Asp Ala Leu Thr Leu Ser Ser Ala Met Trp
595 600 605
Phe Ser Trp Gly Val Leu Leu Asn Ser Gly Ile Gly Glu Gly Ala Pro
610 615 620
Arg Ser Phe Ser Ala Arg Ile Leu Gly Met Val Trp Ala Gly Phe Ala
625 630 635 640
Met Ile Ile Val Ala Ser Tyr Thr Ala Asn Leu Ala Ala Phe Leu Val
645 650 655
Leu Asp Arg Pro Glu Glu Arg Ile Thr Gly Ile Asn Asp Pro Arg Leu
660 665 670
Arg Asn Pro Ser Asp Lys Phe Ile Tyr Ala Thr Val Lys Gln Ser Ser
675 680 685
Val Asp Ile Tyr Phe Arg Arg Gln Val Glu Leu Ser Thr Met Tyr Arg
690 695 700
His Met Glu Lys His Asn Tyr Glu Ser Ala Ala Glu Ala Ile Gln Ala
705 710 715 720
Val Arg Asp Asn Lys Leu His Ala Phe Ile Trp Asp Ser Ala Val Leu
725 730 735
Glu Phe Glu Ala Ser Gln Lys Cys Asp Leu Val Thr Thr Gly Glu Leu
740 745 750
Phe Phe Arg Ser Gly Phe Gly Ile Gly Met Arg Lys Asp Ser Pro Trp
755 760 765
Lys Gln Asn Val Ser Leu Ser Ile Leu Lys Ser His Glu Asn Gly Phe
770 775 780
Met Glu Asp Leu Asp Lys Thr Trp Val Arg Tyr Gln Glu Cys Asp Ser
785 790 795 800
Arg Ser Asn Ala Pro Ala Thr Leu Thr Phe Glu Asn Met Ala Gly Val
805 810 815
Phe Met Leu Val Ala Gly Gly Ile Val Ala Gly Ile Phe Leu Ile Phe
820 825 830
Ile Glu Ile Ala Tyr Lys Arg His Lys Asp Ala Arg Arg Lys Gln Met
835 840 845
Gln Leu Ala Phe Ala Ala Val Asn Val Trp Arg Lys Asn Leu Gln Asp

850

855

860

Arg Lys Ser Gly Arg Ala Glu Pro Asp Pro Lys Lys Lys Ala Thr Phe
865 870 875 880

Arg Ala Ile Thr Ser Thr Leu Ala Ser Ser Phe Lys Arg Arg Arg Ser
885 890 895

Ser Lys Asp Thr Gln Tyr His Pro Thr Asp Ile Thr Gly Pro Leu Asn
900 905 910

Leu Ser Asp Pro Ser Val Ser Thr Val Val
915 920

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3211 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 262..3192

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

CAAGCCGGGC GTTCGGAGCT GTGCCGGCC CCGCTTCAGC ACCGCGGACA GCGCCGGCCG	60
CGTGGGGCTG AGCGCCGAGC CCCCAGCGAC GCTTCAGCCC CCCTTCCCTC GGCCGACGTC	120
CCGGGACCGC CGCTCCGGGG GAGACGTGGC GTCCGCAGCC CGCGGGGCCG GGCGAGCGCA	180
GGACGGCCCG GAAGCCCCGC GGGGGATGCG CCGAGGGCCC CGCGTTCGCG CCGCGCAGAG	240
CCAGGGCCCGC GGCCCGAGCC C ATG AGC ACC ATG CGC CTG CTG ACG CTC GCC Met Ser Thr Met Arg Leu Leu Thr Leu Ala	291
1 5 10	
CTG CTG TTC TCC TCC GTC GCC CGT GCC GCG TGC GAC CCC AAG ATC Leu Leu Phe Ser Cys Ser Val Ala Arg Ala Cys Asp Pro Lys Ile	339
15 20 25	
GTC AAC ATT GGC GCG GTG CTG AGC ACG CGG AAG CAC GAG CAG ATG TTC Val Asn Ile Gly Ala Val Leu Ser Thr Arg Lys His Glu Gln Met Phe	387
30 35 40	
CGC GAG GCC GTG AAC CAG GCC AAC AAG CGG CAC GGC TCC TGG AAG ATT Arg Glu Ala Val Asn Gln Ala Asn Lys Arg His Gly Ser Trp Lys Ile	435
45 50 55	
CAG CTC AAT GCC ACC TCC GTC ACG CAC AAG CCC AAC GCC ATC CAG ATG Gln Leu Asn Ala Thr Ser Val Thr His Lys Pro Asn Ala Ile Gln Met	483
60 65 70	
GCT CTG TCG GTG TGC GAG GAC CTC ATC TCC AGC CAG GTC TAC GCC ATC Ala Leu Ser Val Cys Glu Asp Leu Ile Ser Ser Gln Val Tyr Ala Ile	531
75 80 85 90	
CTA GTT AGC CAT CCA CCT ACC CCC AAC GAC CAC TTC ACT CCC ACC CCT	579

Leu Val Ser His Pro Pro Thr Pro Asn Asp His Phe Thr Pro Thr Pro		
95	100	105
GTC TCC TAC ACA GCC GGC TTC TAC CGC ATA CCC GTG CTG GGG CTG ACC		627
Val Ser Tyr Thr Ala Gly Phe Tyr Arg Ile Pro Val Leu Gly Leu Thr		
110	115	120
ACC CGC ATG TCC ATC TAC TCG GAC AAG AGC ATC CAC CTG AGC TTC CTG		675
Thr Arg Met Ser Ile Tyr Ser Asp Lys Ser Ile His Leu Ser Phe Leu		
125	130	135
CGC ACC GTG CCG CCC TAC TCC CAC CAG TCC AGC GTG TGG TTT GAG ATG		723
Arg Thr Val Pro Pro Tyr Ser His Gln Ser Ser Val Trp Phe Glu Met		
140	145	150
ATG CGT GTC TAC AGC TGG AAC CAC ATC ATC CTG CTG GTC AGC GAC GAC		771
Met Arg Val Tyr Ser Trp Asn His Ile Ile Leu Leu Val Ser Asp Asp		
155	160	165
170		
CAC GAG GGC CGG GCG GCT CAG AAA CGC CTG GAG ACG CTG CTG GAG GAG		819
His Glu Gly Arg Ala Ala Gln Lys Arg Leu Glu Thr Leu Leu Glu Glu		
175	180	185
CGT GAG TCC AAG GCA GAG AAG GTG CTG CAG TTT GAC CCA GGG ACC AAG		867
Arg Glu Ser Lys Ala Glu Lys Val Leu Gln Phe Asp Pro Gly Thr Lys		
190	195	200
AAC GTG ACG GCC CTG CTG ATG GAG GCG AAA GAG CTG GAG GCC CGG GTC		915
Asn Val Thr Ala Leu Leu Met Glu Ala Lys Glu Leu Glu Ala Arg Val		
205	210	215
ATC ATC CTT TCT GCC AGC GAG GAC GAT GCT GCC ACT GTA TAC CGC GCA		963
Ile Ile Leu Ser Ala Ser Glu Asp Asp Ala Ala Thr Val Tyr Arg Ala		
220	225	230
GCC GCG ATG CTG AAC ATG ACG GGC TCC GGG TAC GTG TGG CTG GTC GGC		1011
Ala Ala Met Leu Asn Met Thr Gly Ser Gly Tyr Val Trp Leu Val Gly		
235	240	245
250		
GAG CGC GAG ATC TCG GGG AAC GCC CTG CGC TAC GCC CCA GAC GGC ATC		1059
Glu Arg Glu Ile Ser Gly Asn Ala Leu Arg Tyr Ala Pro Asp Gly Ile		
255	260	265
CTC GGG CTG CAG CTC ATC AAC GGC AAG AAC GAG TCG GCC CAC ATC AGC		1107
Leu Gly Leu Gln Leu Ile Asn Gly Lys Asn Glu Ser Ala His Ile Ser		
270	275	280
GAC GCC GTG GGC GTG GTG GCC CAG GCC GTG CAC GAG CTC CTC GAG AAG		1155
Asp Ala Val Gly Val Val Ala Gln Ala Val His Glu Leu Leu Glu Lys		
285	290	295
GAG AAC ATC ACC GAC CCG CCG CGG GGC TGC GTG GGC AAC ACC AAC ATC		1203
Glu Asn Ile Thr Asp Pro Pro Arg Gly Cys Val Gly Asn Thr Asn Ile		
300	305	310
TGG AAG ACC GGG CCG CTC TTC AAG AGA GTG CTG ATG TCT TCC AAG TAT		1251
Trp Lys Thr Gly Pro Leu Phe Lys Arg Val Leu Met Ser Ser Lys Tyr		
315	320	325
330		
GCG GAT GGG GTG ACT GGT CGC GTG GAG TTC AAT GAG GAT GGG GAC CGG		1299
Ala Asp Gly Val Thr Gly Arg Val Glu Phe Asn Glu Asp Gly Asp Arg		
335	340	345
AAG TTC GCC AAC TAC AGC ATC ATG AAC CTG CAG AAC CGC AAG CTG GTG		1347
Lys Phe Ala Asn Tyr Ser Ile Met Asn Leu Gln Asn Arg Lys Leu Val		

350	355	360	
CAA GTG GGC ATC TAC AAT GGC ACC CAC GTC ATC CCT AAT GAC AGG AAG Gln Val Gly Ile Tyr Asn Gly Thr His Val Ile Pro Asn Asp Arg Lys 365 370 375			1395
ATC ATC TGG CCA GGC GGA GAG ACA GAG AAG CCT CGA GGG TAC CAG ATG Ile Ile Trp Pro Gly Gly Glu Thr Glu Lys Pro Arg Gly Tyr Gln Met 380 385 390			1443
TCC ACC AGA CTG AAG ATT GTG ACG ATC CAC CAG GAG CCC TTC GTG TAC Ser Thr Arg Leu Lys Ile Val Thr Ile His Gln Glu Pro Phe Val Tyr 395 400 405 410			1491
GTC AAG CCC ACG CTG AGT GAT GGG ACA TGC AAG GAG GAG TTC ACA GTC Val Lys Pro Thr Leu Ser Asp Gly Thr Cys Lys Glu Glu Phe Thr Val 415 420 425			1539
AAC GGC GAC CCA GTC AAG AAG GTG ATC TGC ACC GGG CCC AAC GAC ACG Asn Gly Asp Pro Val Lys Lys Val Ile Cys Thr Gly Pro Asn Asp Thr 430 435 440			1587
TCG CCG GGC AGC CCC CGC CAC ACG GTG CCT CAG TGT TGC TAC GGC TTT Ser Pro Gly Ser Pro Arg His Thr Val Pro Gln Cys Cys Tyr Gly Phe 445 450 455			1635
TGC ATC GAC CTG CTC ATC AAG CTG GCA CGG ACC ATG AAC TTC ACC TAC Cys Ile Asp Leu Leu Ile Lys Leu Ala Arg Thr Met Asn Phe Thr Tyr 460 465 470			1683
GAG GTG CAC CTG GTG GCA GAT GGC AAG TTC GGC ACA CAG GAG CGG GTG Glu Val His Leu Val Ala Asp Gly Lys Phe Gly Thr Gln Glu Arg Val 475 480 485 490			1731
AAC AAC AGC AAC AAG AAG GAG TGG AAT GGG ATG ATG GGC GAG CTG CTC Asn Asn Ser Asn Lys Lys Glu Trp Asn Gly Met Met Gly Glu Leu Leu 495 500 505			1779
AGC GGG CAG GCA GAC ATG ATC GTG GCG CCG CTA ACC ATA AAC AAC GAG Ser Gly Gln Ala Asp Met Ile Val Ala Pro Leu Thr Ile Asn Asn Glu 510 515 520			1827
CGC GCG CAG TAC ATC GAG TTT TCC AAG CCC TTC AAG TAC CAG GGC CTG Arg Ala Gln Tyr Ile Glu Phe Ser Lys Pro Phe Lys Tyr Gln Gly Leu 525 530 535			1875
ACT ATT CTG GTC AAG AAG GAG ATT CCC CGG AGC ACG CTG GAC TCG TTC Thr Ile Leu Val Lys Lys Glu Ile Pro Arg Ser Thr Leu Asp Ser Phe 540 545 550			1923
ATG CAG CCG TTC CAG AGC ACA CTG TGG CTG CTG GTG GGG CTG TCG GTG Met Gln Pro Phe Gln Ser Thr Leu Trp Leu Leu Val Gly Leu Ser Val 555 560 565 570			1971
CAC GTG GTG GCC GTG ATG CTG TAC CTG CTG GAC CGC TTC AGC CCC TTC His Val Val Ala Val Met Leu Tyr Leu Leu Asp Arg Phe Ser Pro Phe 575 580 585			2019
GGC CGG TTC AAG GTG AAC AGC GAG GAG GAG GAG GAG GAC GCA CTG ACC Gly Arg Phe Lys Val Asn Ser Glu Glu Glu Glu Asp Ala Leu Thr 590 595 600			2067
CTG TCC TCG GCC ATG TGG TTC TCC TGG GGC GTC CTG CTG AAC TCC GGC Leu Ser Ser Ala Met Trp Phe Ser Trp Gly Val Leu Leu Asn Ser Gly 605 610 615			2115
ATC GGG GAA GGC GCC CCC AGA AGC TTC TCA GCG CGC ATC CTG GGC ATG			2163

Ile	Gly	Glu	Gly	Ala	Pro	Arg	Ser	Phe	Ser	Ala	Arg	Ile	Leu	Gly	Met
620		615						615			630				
GTG	TGG	GCC	GGC	TTT	GCC	ATG	ATC	ATC	GTG	GCC	TCC	TAC	ACC	GCC	AAC
Val	Trp	Ala	Gly	Phe	Ala	Met	Ile	Ile	Val	Ala	Ser	Tyr	Thr	Ala	Asn
635				640					645					650	
CTG	GCG	GCC	TTC	CTG	GTG	CTG	GAC	CGG	CCG	GAG	GAG	CGC	ATC	ACG	GGC
Leu	Ala	Ala	Phe	Leu	Val	Leu	Asp	Arg	Pro	Glu	Glu	Arg	Ile	Thr	Gly
				655					660				665		
ATC	AAC	GAC	CCT	CGG	CTG	AGG	AAC	CCC	TCG	GAC	AAG	TTT	ATC	TAC	GCC
Ile	Asn	Asp	Pro	Arg	Leu	Arg	Asn	Pro	Ser	Asp	Lys	Phe	Ile	Tyr	Ala
			670				675					680			
ACG	GTG	AAG	CAG	AGC	TCC	GTG	GAT	ATC	TAC	TTC	CGG	CGC	CAG	GTG	GAG
Thr	Val	Lys	Gln	Ser	Ser	Val	Asp	Ile	Tyr	Phe	Arg	Arg	Gln	Val	Glu
		685				690					695				
CTG	AGC	ACC	ATG	TAC	CGG	CAT	ATG	GAG	AAG	CAC	AAC	TAC	GAG	AGT	GCG
Leu	Ser	Thr	Met	Tyr	Arg	His	Met	Glu	Lys	His	Asn	Tyr	Glu	Ser	Ala
			700			705					710				
GCG	GAG	GCC	ATC	CAG	GCC	GTG	AGA	GAC	AAC	AAG	CTG	CAT	GCC	TTC	ATC
Ala	Glu	Ala	Ile	Gln	Ala	Val	Arg	Asp	Asn	Lys	Leu	His	Ala	Phe	Ile
			715		720					725				730	
TGG	GAC	TCG	GCG	GTG	CTG	GAG	TTC	GAG	GCC	TCG	CAG	AAG	TGC	GAC	CTG
Trp	Asp	Ser	Ala	Val	Leu	Glu	Phe	Glu	Ala	Ser	Gln	Lys	Cys	Asp	Leu
			735			740					745				
GTG	ACG	ACT	GGA	GAG	CTG	TTT	TTC	CGC	TCG	GGC	TTC	GGC	ATA	GGG	ATG
Val	Thr	Thr	Gly	Glu	Leu	Phe	Phe	Arg	Ser	Gly	Phe	Gly	Ile	Gly	Met
			750			755					760				
CGC	AAA	GAC	AGC	CCC	TGG	AAG	CAG	AAC	GTC	TCC	CTG	TCC	ATC	CTC	AAG
Arg	Lys	Asp	Ser	Pro	Trp	Lys	Gln	Asn	Val	Ser	Leu	Ser	Ile	Leu	Lys
			765			770					775				
TCC	CAC	GAG	AAT	GGC	TTC	ATG	GAA	GAC	CTG	GAC	AAG	ACG	TGG	GTT	CGG
Ser	His	Glu	Asn	Gly	Phe	Met	Glu	Asp	Leu	Asp	Lys	Thr	Trp	Val	Arg
			780		785					790					
TAT	CAG	GAA	TGT	GAC	TCG	CGC	AGC	AAC	GCC	CCT	GCG	ACC	CTT	ACT	TTT
Tyr	Gln	Glu	Cys	Asp	Ser	Arg	Ser	Asn	Ala	Pro	Ala	Thr	Leu	Thr	Phe
			795		800					805				810	
GAG	AAC	ATG	GCC	GGG	GTC	TTC	ATG	CTG	GTA	GCT	GGG	GGC	ATC	GTG	GCC
Glu	Asn	Met	Ala	Gly	Val	Phe	Met	Leu	Val	Ala	Gly	Gly	Ile	Val	Ala
			815			820					825				
GGG	ATC	TTC	CTG	ATT	TTC	ATC	GAG	ATT	GCC	TAC	AAG	CGG	CAC	AAG	GAT
Gly	Ile	Phe	Leu	Ile	Phe	Ile	Glu	Ile	Ala	Tyr	Lys	Arg	His	Lys	Asp
			830			835					840				
GCT	CGC	CGG	AAG	CAG	ATG	CAG	CTG	GCC	TTT	GCC	GCC	GTT	AAC	GTG	TGG
Ala	Arg	Arg	Lys	Gln	Met	Gln	Leu	Ala	Phe	Ala	Ala	Val	Asn	Val	Trp
			845			850					855				
CGG	AAG	AAC	CTG	CAG	GAT	AGA	AAG	AGT	GGT	AGA	GCA	GAG	CCT	GAC	CCT
Arg	Lys	Asn	Leu	Gln	Asp	Arg	Lys	Ser	Gly	Arg	Ala	Glu	Pro	Asp	Pro
			860			865					870				
AAA	AAG	AAA	GCC	ACA	TTT	AGG	GCT	ATC	ACC	TCC	ACC	CTG	GCT	TCC	AGC
Lys	Lys	Ala	Thr	Phe	Arg	Ala	Ile	Thr	Ser	Thr	Leu	Ala	Ser	Ser	
			875			880					885			890	

TTC AAG AGG CGT AGG TCC TCC AAA GAC ACG CTG GCT CGG GAC TGT CTT Phe Lys Arg Arg Arg Ser Ser Lys Asp Thr Leu Ala Arg Asp Cys Leu 895 900 905	2979
CAA CCC TGC CCT GCA CCT TGG GCA CGG GAG AGC GCC ACC CGC CCG CCC Gln Pro Cys Pro Ala Pro Trp Ala Arg Glu Ser Ala Thr Arg Pro Pro 910 915 920	3027
CCG CCC TCG CTC CGG GTG CGT GAC CGG CCC GCC ACC TTG TAC AGA ACC Pro Pro Ser Leu Arg Val Arg Asp Arg Pro Ala Thr Leu Tyr Arg Thr 925 930 935	3075
AGC ACT CCC AGG GCC CGA GCG CGT GCC TTC CCC GTG CGC AGC CGC GCT Ser Thr Pro Arg Ala Arg Ala Phe Pro Val Arg Ser Arg Ala 940 945 950	3123
CTG CCC CTC CGT CCC CAG GGT GCA GGC GCG CAC CGC CCA ACC CCC ACC Leu Pro Leu Arg Pro Gln Gly Ala Gly Ala His Arg Pro Thr Pro Thr 955 960 965 970	3171
TCC CGG TGT ATG CAG TGG TGATGCCTAA AGGAATGTCA CG Ser Arg Cys Met Gln Trp 975	3211

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 976 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Met Ser Thr Met Arg Leu Leu Thr Leu Ala Leu Leu Phe Ser Cys Ser 1 5 10 15
Val Ala Arg Ala Ala Cys Asp Pro Lys Ile Val Asn Ile Gly Ala Val 20 25 30
Leu Ser Thr Arg Lys His Glu Gln Met Phe Arg Glu Ala Val Asn Gln 35 40 45
Ala Asn Lys Arg His Gly Ser Trp Lys Ile Gln Leu Asn Ala Thr Ser 50 55 60
Val Thr His Lys Pro Asn Ala Ile Gln Met Ala Leu Ser Val Cys Glu 65 70 75 80
Asp Leu Ile Ser Ser Gln Val Tyr Ala Ile Leu Val Ser His Pro Pro 85 90 95
Thr Pro Asn Asp His Phe Thr Pro Thr Pro Val Ser Tyr Thr Ala Gly 100 105 110
Phe Tyr Arg Ile Pro Val Leu Gly Leu Thr Thr Arg Met Ser Ile Tyr 115 120 125
Ser Asp Lys Ser Ile His Leu Ser Phe Leu Arg Thr Val Pro Pro Tyr 130 135 140
Ser His Gln Ser Ser Val Trp Phe Glu Met Met Arg Val Tyr Ser Trp 145 150 155 160
Asn His Ile Ile Leu Leu Val Ser Asp Asp His Glu Gly Arg Ala Ala

165	170	175
Gln Lys Arg Leu Glu Thr Leu Leu Glu Glu Arg Glu Ser Lys Ala Glu		
180	185	190
Lys Val Leu Gln Phe Asp Pro Gly Thr Lys Asn Val Thr Ala Leu Leu		
195	200	205
Met Glu Ala Lys Glu Leu Glu Ala Arg Val Ile Ile Leu Ser Ala Ser		
210	215	220
Glu Asp Asp Ala Ala Thr Val Tyr Arg Ala Ala Ala Met Leu Asn Met		
225	230	235
240		
Thr Gly Ser Gly Tyr Val Trp Leu Val Gly Glu Arg Glu Ile Ser Gly		
245	250	255
Asn Ala Leu Arg Tyr Ala Pro Asp Gly Ile Leu Gly Leu Gln Leu Ile		
260	265	270
Asn Gly Lys Asn Glu Ser Ala His Ile Ser Asp Ala Val Gly Val Val		
275	280	285
Ala Gln Ala Val His Glu Leu Glu Lys Glu Asn Ile Thr Asp Pro		
290	295	300
Pro Arg Gly Cys Val Gly Asn Thr Asn Ile Trp Lys Thr Gly Pro Leu		
305	310	315
320		
Phe Lys Arg Val Leu Met Ser Ser Lys Tyr Ala Asp Gly Val Thr Gly		
325	330	335
Arg Val Glu Phe Asn Glu Asp Gly Asp Arg Lys Phe Ala Asn Tyr Ser		
340	345	350
Ile Met Asn Leu Gln Asn Arg Lys Leu Val Gln Val Gly Ile Tyr Asn		
355	360	365
Gly Thr His Val Ile Pro Asn Asp Arg Lys Ile Ile Trp Pro Gly Gly		
370	375	380
Glu Thr Glu Lys Pro Arg Gly Tyr Gln Met Ser Thr Arg Leu Lys Ile		
385	390	395
400		
Val Thr Ile His Gln Glu Pro Phe Val Tyr Val Lys Pro Thr Leu Ser		
405	410	415
Asp Gly Thr Cys Lys Glu Glu Phe Thr Val Asn Gly Asp Pro Val Lys		
420	425	430
Lys Val Ile Cys Thr Gly Pro Asn Asp Thr Ser Pro Gly Ser Pro Arg		
435	440	445
His Thr Val Pro Gln Cys Cys Tyr Gly Phe Cys Ile Asp Leu Leu Ile		
450	455	460
Lys Leu Ala Arg Thr Met Asn Phe Thr Tyr Glu Val His Leu Val Ala		
465	470	475
480		
Asp Gly Lys Phe Gly Thr Gln Glu Arg Val Asn Asn Ser Asn Lys Lys		
485	490	495
Glu Trp Asn Gly Met Met Gly Glu Leu Leu Ser Gly Gln Ala Asp Met		
500	505	510
Ile Val Ala Pro Leu Thr Ile Asn Asn Glu Arg Ala Gln Tyr Ile Glu		

515

520

525

Phe Ser Lys Pro Phe Lys Tyr Gln Gly Leu Thr Ile Leu Val Lys Lys
530 535 540

Glu Ile Pro Arg Ser Thr Leu Asp Ser Phe Met Gln Pro Phe Gln Ser
545 550 555 560

Thr Leu Trp Leu Leu Val Gly Leu Ser Val His Val Val Ala Val Met
565 570 575

Leu Tyr Leu Leu Asp Arg Phe Ser Pro Phe Gly Arg Phe Lys Val Asn
580 585 590

Ser Glu Glu Glu Glu Asp Ala Leu Thr Leu Ser Ser Ala Met Trp
595 600 605

Phe Ser Trp Gly Val Leu Leu Asn Ser Gly Ile Gly Glu Gly Ala Pro
610 615 620

Arg Ser Phe Ser Ala Arg Ile Leu Gly Met Val Trp Ala Gly Phe Ala
625 630 635 640

Met Ile Ile Val Ala Ser Tyr Thr Ala Asn Leu Ala Ala Phe Leu Val
645 650 655

Leu Asp Arg Pro Glu Glu Arg Ile Thr Gly Ile Asn Asp Pro Arg Leu
660 665 670

Arg Asn Pro Ser Asp Lys Phe Ile Tyr Ala Thr Val Lys Gln Ser Ser
675 680 685

Val Asp Ile Tyr Phe Arg Arg Gln Val Glu Leu Ser Thr Met Tyr Arg
690 695 700

His Met Glu Lys His Asn Tyr Glu Ser Ala Ala Glu Ala Ile Gln Ala
705 710 715 720

Val Arg Asp Asn Lys Leu His Ala Phe Ile Trp Asp Ser Ala Val Leu
725 730 735

Glu Phe Glu Ala Ser Gln Lys Cys Asp Leu Val Thr Thr Gly Glu Leu
740 745 750

Phe Phe Arg Ser Gly Phe Gly Ile Gly Met Arg Lys Asp Ser Pro Trp
755 760 765

Lys Gln Asn Val Ser Leu Ser Ile Leu Lys Ser His Glu Asn Gly Phe
770 775 780

Met Glu Asp Leu Asp Lys Thr Trp Val Arg Tyr Gln Glu Cys Asp Ser
785 790 795 800

Arg Ser Asn Ala Pro Ala Thr Leu Thr Phe Glu Asn Met Ala Gly Val
805 810 815

Phe Met Leu Val Ala Gly Gly Ile Val Ala Gly Ile Phe Leu Ile Phe
820 825 830

Ile Glu Ile Ala Tyr Lys Arg His Lys Asp Ala Arg Arg Lys Gln Met
835 840 845

Gln Leu Ala Phe Ala Ala Val Asn Val Trp Arg Lys Asn Leu Gln Asp
850 855 860

Arg Lys Ser Gly Arg Ala Glu Pro Asp Pro Lys Lys Lys Ala Thr Phe

865	870	875	880
Arg Ala Ile Thr Ser Thr Leu Ala Ser Ser Phe Lys Arg Arg Arg Ser			
885	890	895	
Ser Lys Asp Thr Leu Ala Arg Asp Cys Leu Gln Pro Cys Pro Ala Pro			
900	905	910	
Trp Ala Arg Glu Ser Ala Thr Arg Pro Pro Pro Pro Ser Leu Arg Val			
915	920	925	
Arg Asp Arg Pro Ala Thr Leu Tyr Arg Thr Ser Thr Pro Arg Ala Arg			
930	935	940	
Ala Arg Ala Phe Pro Val Arg Ser Arg Ala Leu Pro Leu Arg Pro Gln			
945	950	955	960
Gly Ala Gly Ala His Arg Pro Thr Pro Thr Ser Arg Cys Met Gln Trp			
965	970	975	

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4361 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 262..3141

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

CAAGCCGGGC GTTCGGAGCT GTGCCCGGCC CCGCTTCAGC ACCGGGACA GCGCCGGCCG	60
CGTGGGGCTG AGCGCCGAGC CCCCGCGCAC GCTTCAGCCC CCCTTCCTC GGCCGACGTC	120
CCGGGACCGC CGCTCCGGGG GAGACGTGGC GTCCGCAGCC CGCGGGGCCG GGCGAGCGCA	180
GGACGGCCCG GAAGCCCCGC GGGGGATGCG CCGAGGGCCC CGCGTTCGCG CCGCGCAGAG	240
CCAGGCCCGC GGCCCGAGCC C ATG AGC ACC ATG CGC CTG CTG ACG CTC GCC	291
Met Ser Thr Met Arg Leu Leu Thr Leu Ala	
1 5 10	
CTG CTG TTC TCC TGC TCC GTC GCC CGT GCC GCG TGC GAC CCC AAG ATC	339
Leu Leu Phe Ser Cys Ser Val Ala Arg Ala Ala Cys Asp Pro Lys Ile	
15 20 25	
GTC AAC ATT GGC GCG GTG CTG AGC ACG CGG AAG CAC GAG CAG ATG TTC	387
Val Asn Ile Gly Ala Val Leu Ser Thr Arg Lys His Glu Gin Met Phe	
30 35 40	
CGC GAG GCC GTG AAC CAG GCC AAC AAG CGG CAC GGC TCC TGG AAG ATT	435
Arg Glu Ala Val Asn Gln Ala Asn Lys Arg His Gly Ser Trp Lys Ile	
45 50 55	

CAG CTC AAT GCC ACC TCC GTC ACG CAC AAG CCC AAC GCC ATC CAG ATG	483
Gln Leu Asn Ala Thr Ser Val Thr His Lys Pro Asn Ala Ile Gln Met	
60 65 70	
GCT CTG TCG GTG TGC GAG GAC CTC ATC TCC AGC CAG GTC TAC GCC ATC	531
Ala Leu Ser Val Cys Glu Asp Leu Ile Ser Ser Gln Val Tyr Ala Ile	
75 80 85 90	
CTA GTT AGC CAT CCA CCT ACC CCC AAC GAC CAC TTC ACT CCC ACC CCT	579
Leu Val Ser His Pro Pro Thr Pro Asn Asp His Phe Thr Pro Thr Pro	
95 100 105	
GTC TCC TAC ACA GCC GGC TTC TAC CGC ATA CCC GTG CTG GGG CTG ACC	627
Val Ser Tyr Thr Ala Gly Phe Tyr Arg Ile Pro Val Leu Gly Leu Thr	
110 115 120	
ACC CGC ATG TCC ATC TAC TCG GAC AAG AGC ATC CAC CTG AGC TTC CTG	675
Thr Arg Met Ser Ile Tyr Ser Asp Lys Ser Ile His Leu Ser Phe Leu	
125 130 135	
CGC ACC GTG CCG CCC TAC TCC CAC CAG TCC AGC GTG TGG TTT GAG ATG	723
Arg Thr Val Pro Pro Tyr Ser His Gln Ser Ser Val Trp Phe Glu Met	
140 145 150	
ATG CGT GTC TAC AGC TGG AAC CAC ATC ATC CTG CTG GTC AGC GAC GAC	771
Met Arg Val Tyr Ser Trp Asn His Ile Ile Leu Leu Val Ser Asp Asp	
155 160 165 170	
CAC GAG GGC CGG GCG GCT CAG AAA CGC CTG GAG ACG CTG CTG GAG GAG	819
His Glu Gly Arg Ala Ala Gln Lys Arg Leu Glu Thr Leu Leu Glu Glu	
175 180 185	
CGT GAG TCC AAG AGT AAA AAA AGG AAC TAT GAA AAC CTC GAC CAA CTG	867
Arg Glu Ser Lys Ser Lys Arg Asn Tyr Glu Asn Leu Asp Gln Leu	
190 195 200	
TCC TAT GAC AAC AAG CGC GGA CCC AAG GCA GAG AAG GTG CTG CAG TTT	915
Ser Tyr Asp Asn Lys Arg Gly Pro Lys Ala Glu Lys Val Leu Gln Phe	
205 210 215	
GAC CCA GGG ACC AAG AAC GTG ACG GCC CTG CTG ATG GAG GCG AAA GAG	963
Asp Pro Gly Thr Lys Asn Val Thr Ala Leu Leu Met Glu Ala Lys Glu	
220 225 230	
CTG GAG GCC CGG GTC ATC ATC CTT TCT GCC AGC GAG GAC GAT GCT GCC	1011
Leu Glu Ala Arg Val Ile Ile Leu Ser Ala Ser Glu Asp Asp Ala Ala	
235 240 245 250	
ACT GTA TAC CGC GCA GCC GCG ATG CTG AAC ATG ACG GGC TCC GGG TAC	1059
Thr Val Tyr Arg Ala Ala Ala Met Leu Asn Met Thr Gly Ser Gly Tyr	
255 260 265	
GTC TGG CTG GTC GGC GAG CGC GAG ATC TCG GGG AAC GCC CTG CGC TAC	1107
Val Trp Leu Val Gly Glu Arg Glu Ile Ser Gly Asn Ala Leu Arg Tyr	
270 275 280	
GCC CCA GAC GGC ATC CTC GGG CTG CAG CTC ATC AAC GGC AAG AAC GAG	1155
Ala Pro Asp Gly Ile Leu Gly Leu Gln Leu Ile Asn Gly Lys Asn Glu	
285 290 295	
TCG GCC CAC ATC AGC GAC GCC GTG GGC GTG GTG GCC CAG GCC GTG CAC	1203
Ser Ala His Ile Ser Asp Ala Val Gly Val Val Ala Gln Ala Val His	
300 305 310	
GAG CTC CTC GAG AAG GAG AAC ATC ACC GAC CCG CCG CGG GGC TGC GTG	1251
Glu Leu Leu Glu Lys Glu Asn Ile Thr Asp Pro Pro Arg Gly Cys Val	
315 320 325 330	

GGC AAC ACC AAC ATC TGG AAG ACC GGG CCG CTC TTC AAG AGA GTG CTG Gly Asn Thr Asn Ile Trp Lys Thr Gly Pro Leu Phe Lys Arg Val Leu 335 340 345	1299
ATG TCT TCC AAG TAT GCG GAT GGG GTG ACT GGT CGC GTG GAG TTC AAT Met Ser Ser Lys Tyr Ala Asp Gly Val Thr Gly Arg Val Glu Phe Asn 350 355 360	1347
GAG GAT GGG GAC CGG AAG TTC GCC AAC TAC AGC ATC ATG AAC CTG CAG Glu Asp Gly Asp Arg Lys Phe Ala Asn Tyr Ser Ile Met Asn Leu Gln 365 370 375	1395
AAC CGC AAG CTG GTG CAA GTG GGC ATC TAC AAT GGC ACC CAC GTC ATC Asn Arg Lys Leu Val Gln Val Gly Ile Tyr Asn Gly Thr His Val Ile 380 385 390	1443
CCT AAT GAC AGG AAG ATC ATC TGG CCA GGC GGA GAG ACA GAG AAG CCT Pro Asn Asp Arg Lys Ile Ile Trp Pro Gly Gly Glu Thr Glu Lys Pro 395 400 405 410	1491
CGA GGG TAC CAG ATG TCC ACC AGA CTG AAG ATT GTG ACG ATC CAC CAG Arg Gly Tyr Gln Met Ser Thr Arg Leu Lys Ile Val Thr Ile His Gln 415 420 425	1539
GAG CCC TTC GTG TAC GTC AAG CCC ACG CTG AGT GAT GGG ACA TGC AAG Glu Pro Phe Val Tyr Val Lys Pro Thr Leu Ser Asp Gly Thr Cys Lys 430 435 440	1587
GAG GAG TTC ACA GTC AAC GGC GAC CCA GTC AAG AAG GTG ATC TGC ACC Glu Glu Phe Thr Val Asn Gly Asp Pro Val Lys Lys Val Ile Cys Thr 445 450 455	1635
GGG CCC AAC GAC ACG TCG CCG GGC AGC CCC CGC CAC ACG GTG CCT CAG Gly Pro Asn Asp Thr Ser Pro Gly Ser Pro Arg His Thr Val Pro Gln 460 465 470	1683
TGT TGC TAC GGC TTT TGC ATC GAC CTG CTC ATC AAG CTG GCA CGG ACC Cys Cys Tyr Gly Phe Cys Ile Asp Leu Leu Ile Lys Leu Ala Arg Thr 475 480 485 490	1731
ATG AAC TTC ACC TAC GAG GTG CAC CTG GTG GCA GAT GGC AAG TTC GGC Met Asn Phe Thr Tyr Glu Val His Leu Val Ala Asp Gly Lys Phe Gly 495 500 505	1779
ACA CAG GAG CGG GTG AAC AAC AGC AAC AAG AAG GAG TGG AAT GGG ATG Thr Gln Glu Arg Val Asn Asn Ser Asn Lys Lys Glu Trp Asn Gly Met 510 515 520	1827
ATG GGC GAG CTG CTC AGC GGG CAG GCA GAC ATG ATC GTG GCG CCG CTA Met Gly Glu Leu Leu Ser Gly Gln Ala Asp Met Ile Val Ala Pro Leu 525 530 535	1875
ACC ATA AAC AAC GAG CGC GCG CAG TAC ATC GAG TTT TCC AAG CCC TTC Thr Ile Asn Asn Glu Arg Ala Gln Tyr Ile Glu Phe Ser Lys Pro Phe 540 545 550	1923
AAG TAC CAG GGC CTG ACT ATT CTG GTC AAG AAG GAG ATT CCC CGG AGC Lys Tyr Gln Gly Leu Thr Ile Leu Val Lys Lys Glu Ile Pro Arg Ser 555 560 565 570	1971
ACG CTG GAC TCG TTC ATG CAG CCG TTC CAG AGC ACA CTG TGG CTG CTG Thr Leu Asp Ser Phe Met Gln Pro Phe Gln Ser Thr Leu Trp Leu Leu 575 580 585	2019
GTG GGG CTG TCG GTG CAC GTG GTG GCC GTG ATG CTG TAC CTG CTG GAC Val Gly Leu Ser Val His Val Ala Val Met Leu Tyr Leu Leu Asp 590 595 600	2067

CGC TTC AGC CCC TTC GGC CGG TTC AAG GTG AAC AGC GAG GAG GAG GAG Arg Phe Ser Pro Phe Gly Arg Phe Lys Val Asn Ser Glu Glu Glu Glu 605 610 615	2115
GAG GAC GCA CTG ACC CTG TCC TCG GCC ATG TGG TTC TCC TGG GGC GTC Glu Asp Ala Leu Thr Leu Ser Ser Ala Met Trp Phe Ser Trp Gly Val 620 625 630	2163
CTG CTC AAC TCC GGC ATC GGG GAA GGC GCC CCC AGA AGC TTC TCA GCG Leu Leu Asn Ser Gly Ile Gly Glu Gly Ala Pro Arg Ser Phe Ser Ala 635 640 645 650	2211
CGC ATC CTG GGC ATG GTG TGG GCC GGC TTT GCC ATG ATC ATC GTG GCC Arg Ile Leu Gly Met Val Trp Ala Gly Phe Ala Met Ile Ile Val Ala 655 660 665	2259
TCC TAC ACC GCC AAC CTG GCG GCC TTC CTG GTG CTG GAC CGG CCG GAG Ser Tyr Thr Ala Asn Leu Ala Phe Leu Val Leu Asp Arg Pro Glu 670 675 680	2307
GAG CCG ATC ACG GGC ATC AAC GAC CCT CGG CTG AGG AAC CCC TCG GAC Glu Arg Ile Thr Gly Ile Asn Asp Pro Arg Leu Arg Asn Pro Ser Asp 685 690 695	2355
AAG TTT ATC TAC GCC ACG GTG AAG CAG AGC TCC GTG GAT ATC TAC TTC Lys Phe Ile Tyr Ala Thr Val Lys Gln Ser Ser Val Asp Ile Tyr Phe 700 705 710	2403
CGG CGC CAG GTG GAG CTG AGC ACC ATG TAC CGG CAT ATG GAG AAG CAC Arg Arg Gln Val Glu Leu Ser Thr Met Tyr Arg His Met Glu Lys His 715 720 725 730	2451
AAC TAC GAG AGT GCG GCG GAG GCC ATC CAG GCC GTG AGA GAC AAC AAG Asn Tyr Glu Ser Ala Ala Ile Gln Ala Val Arg Asp Asn Lys 735 740 745	2499
CTG CAT GCC TTC ATC TGG GAC TCG GCG GTG CTG GAG TTC GAG GCC TCG Leu His Ala Phe Ile Trp Asp Ser Ala Val Leu Glu Phe Glu Ala Ser 750 755 760	2547
CAG AAG TGC GAC CTG GTG ACG ACT GGA GAG CTG TTT TTC CGC TCG GGC Gln Lys Cys Asp Leu Val Thr Thr Gly Glu Leu Phe Phe Arg Ser GLY 765 770 775	2595
TTC GGC ATA GGC ATG CGC AAA GAC AGC CCC TGG AAG CAG AAC GTC TCC Phe Gly Ile Gly Met Arg Lys Asp Ser Pro Trp Lys Gln Asn Val Ser 780 785 790	2643
CTG TCC ATC CTC AAG TCC CAC GAG AAT GGC TTC ATG GAA GAC CTG GAC Leu Ser Ile Leu Lys Ser His Glu Asn Gly Phe Met Glu Asp Leu Asp 795 800 805 810	2691
AAG ACG TGG GTT CGG TAT CAG GAA TGT GAC TCG CGC AGC AAC GCC CCT Lys Thr Trp Val Arg Tyr Gln Glu Cys Asp Ser Arg Ser Asn Ala Pro 815 820 825	2739
GCG ACC CTT ACT TTT GAG AAC ATG GCC GGG GTC TTC ATG CTG GTA GCT Ala Thr Leu Thr Phe Glu Asn Met Ala Gly Val Phe Met Leu Val Ala 830 835 840	2787
GGG GGC ATC GTG GCC GGG ATC TTC CTG ATT TTC ATC GAG ATT GCC TAC Gly Gly Ile Val Ala Gly Ile Phe Leu Ile Phe Ile Glu Ile Ala Tyr 845 850 855	2835
AAG CGG CAC AAG GAT GCT CGC CGG AAG CAG ATG CAG CTG GCC TTT GCC Lys Arg His Lys Asp Ala Arg Arg Lys Gln Met Gln Leu Ala Phe Ala 860 865 870	2883

GCC GTT AAC GTG TGG CGG AAG AAC CTG CAG GAT AGA AAG AAT	GGT AGA	2931	
Ala Val Asn Val Trp Arg Lys Asn Leu Gln Asp Arg Lys Ser	Ser Trp		
875	880	885	890
GCA GAG CCT GAC CCT AAA AAG AAA GCC ACA TTT AGG GCT ATC ACC	TCC	2979	
Ala Glu Pro Asp Pro Lys Lys Ala Thr Phe Arg Ala Ile Thr	Ser		
895	900	905	
ACC CTG GCT TCC AGC TTC AAG AGG CGT AGG TCC TCC AAA GAC ACG	AGC	3027	
Thr Leu Ala Ser Ser Phe Lys Arg Arg Ser Ser Lys Asp Thr Ser			
910	915	920	
ACC GGG GGT GGA CGC GGT GCT TTG CAA AAC CAA AAA GAC ACA GTG	CTG	3075	
Thr Gly Gly Arg Gly Ala Leu Gln Asn Gln Lys Asp Thr Val Leu			
925	930	935	
CCG CGA CGC GCT ATT GAG AGG GAG GGC CAG CTG CAG CTG TGT	TCC	3123	
Pro Arg Arg Ala Ile Glu Arg Glu Gly Gln Leu Gln Leu Cys Ser			
940	945	950	
CGT CAT AGG GAG AGC TGAGACTCCC CGCCCCGCCCT CCTCTGCCCT	CTCCCCCGCA	3178	
Arg His Arg Glu Ser			
955	960		
GACAGACAGA CAGACGGACG GGACAGCGGC CGGGCCCACG CAGAGCCCCG	GAGCACACG	3238	
GGGTCGGGGG AGGAGCACCC CCAGCCTCCC CCAGGCTGCG CCTGCCGCC	CGCCGGTTGG	3298	
CCGGCTGGCC GGTCCACCCC GTCCCGGCC CGCGCGTGCC CCCAGCGTGG	GGCTAACGGG	3358	
CGCCTTGTCT GTGTATTTCT ATTTTGCAGC AGTACCATCC CACTGATATC	AAGGGCCCGC	3418	
TCAACCTCTC AGATCCCTCG GTCAGCACCG TGGTGTGAGG CCCCGGGAGG	CGCCCAACCTG	3478	
CCCAGTTAGC CCGGCCAAGG ACACTGATGG GTCCTGCTGC TCGGGAAGGC	CTGAGGGAAG	3538	
CCCACCCGCC CCAGAGACTG CCCACCCCTGG GCCTCCCGTC CGTCCGCCG	CCCACCCGCC	3598	
TGCCTGGCGG GCAGCCCCCTG CTGGACCAAG GTGCGGACCG GAGCGGCTGA	GGACGGGGCA	3658	
GAGCTGAGTC GGCTGGCAG GGCGCAGGG CGCTCCGGCA GAGGCAGGCC	CCTGGGGTCT	3718	
CTGAGCAGTG GGGAGCGGGG GCTAACTGCC CCCAGGCCGA GGGGCTTGGG	GCAGAGACGG	3778	
CAGCCCCATC CTTCCCGCAG CACCAGCCTG AGCCACAGTG GGGCCATGG	CCCCAGCTGG	3838	
CTGGGTGCGC CCTCCTCGGG CGCCTGCGCT CCTCTGCAGC CTGAGCTCCA	CCCTCCCCCTC	3898	
TTCTTGCAG ACCGCCAAC AAACACCCCG TCTGCCCTT GACGCCACAC	GCCGGGGCTG	3958	
GCGCTGCCCT CCCCCACGGC CGTCCCTGAC TTCCCAGCTG GCAGCGCCTC	CCGCCGCCCTC	4018	
GGGCCGCCCTC CTCCAGAATC GAGAGGGCTG AGCCCTCCT CTCCTCGTGC	GGCCTCGAGC	4078	
ACAGAAAGGGG GCCTCCCCGG GGGTCCCCGG ACGCTGGCTC GGGACTGTCT	TCAACCTGTC	4138	
CCTGCACCTT GGGCACGGGA GAGCGCCACC CGCCCGCCCC CGCCCTCGCT	CGGGGTGCGT	4198	
GACCGGCCCG CCACCTTGTG CAGAACCAAGC ACTCCCAGGG CCCGAGCGCG	TGCCTTCCCC	4258	
GTGCGCAGCC CGCGCTCTGCC CCTCCGTCCC CAGGGTGCAG GCGCGCACCG	CCCAAACCCCG	4318	
ACCTCCCGT GSTATGCAGTG GTGATGCCTA AAGGAATGTC ACG		4361	

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 959 amino acids
(B) TYPE: amino acid
(C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Met Ser Thr Met Arg Leu Leu Thr Leu Ala Leu Leu Phe Ser Cys Ser
1 5 10 15

Val Ala Arg Ala Ala Cys Asp Pro Lys Ile Val Asn Ile Gly Ala Val
20 25 30

Leu Ser Thr Arg Lys His Glu Gln Met Phe Arg Glu Ala Val Asn Gln
35 40 45

Ala Asn Lys Arg His Gly Ser Trp Lys Ile Gln Leu Asn Ala Thr Ser
50 55 60

Val Thr His Lys Pro Asn Ala Ile Gln Met Ala Leu Ser Val Cys Glu
65 70 75 80

Asp Leu Ile Ser Ser Gln Val Tyr Ala Ile Leu Val Ser His Pro Pro
85 90 95

Thr Pro Asn Asp His Phe Thr Pro Thr Pro Val Ser Tyr Thr Ala Gly
100 105 110

Phe Tyr Arg Ile Pro Val Leu Gly Leu Thr Thr Arg Met Ser Ile Tyr
115 120 125

Ser Asp Lys Ser Ile His Leu Ser Phe Leu Arg Thr Val Pro Pro Tyr
130 135 140

Ser His Gln Ser Ser Val Trp Phe Glu Met Met Arg Val Tyr Ser Trp
145 150 155 160

Asn His Ile Ile Leu Leu Val Ser Asp Asp His Glu Gly Arg Ala Ala
165 170 175

Gln Lys Arg Leu Glu Thr Leu Leu Glu Glu Arg Glu Ser Lys Ser Lys
180 185 190

Lys Arg Asn Tyr Glu Asn Leu Asp Gln Leu Ser Tyr Asp Asn Lys Arg
195 200 205

Gly Pro Lys Ala Glu Lys Val Leu Gln Phe Asp Pro Gly Thr Lys Asn
210 215 220

Val Thr Ala Leu Leu Met Glu Ala Lys Glu Leu Glu Ala Arg Val Ile
225 230 235 240

Ile Leu Ser Ala Ser Glu Asp Asp Ala Ala Thr Val Tyr Arg Ala Ala
245 250 255

Ala Met Leu Asn Met Thr Gly Ser Gly Tyr Val Trp Leu Val Gly Glu
260 265 270

Arg Glu Ile Ser Gly Asn Ala Leu Arg Tyr Ala Pro Asp Gly Ile Leu
275 280 285

Gly Leu Gln Leu Ile Asn Gly Lys Asn Glu Ser Ala His Ile Ser Asp
290 295 300

Ala Val Gly Val Val Ala Gln Ala Val His Glu Leu Leu Glu Lys Glu

305 310 315 320
Asn Ile Thr Asp Pro Pro Arg Gly Cys Val Gly Asn Thr Asn Ile Trp
325 330 335
Lys Thr Gly Pro Leu Phe Lys Arg Val Leu Met Ser Ser Lys Tyr Ala
340 345 350
Asp Gly Val Thr Gly Arg Val Glu Phe Asn Glu Asp Gly Asp Arg Lys
355 360 365

Phe Ala Asn Tyr Ser Ile Met Asn Leu Gln Asn Arg Lys Leu Val Gln
370 375 380
Val Gly Ile Tyr Asn Gly Thr His Val Ile Pro Asn Asp Arg Lys Ile
385 390 395 400
Ile Trp Pro Gly Gly Glu Thr Glu Lys Pro Arg Gly Tyr Gln Met Ser
405 410 415
Thr Arg Leu Lys Ile Val Thr Ile His Gln Glu Pro Phe Val Tyr Val
420 425 430
Lys Pro Thr Leu Ser Asp Gly Thr Cys Lys Glu Glu Phe Thr Val Asn
435 440 445
Gly Asp Pro Val Lys Lys Val Ile Cys Thr Gly Pro Asn Asp Thr Ser
450 455 460
Pro Gly Ser Pro Arg His Thr Val Pro Gln Cys Cys Tyr Gly Phe Cys
465 470 475 480
Ile Asp Leu Leu Ile Lys Leu Ala Arg Thr Met Asn Phe Thr Tyr Glu
485 490 495
Val His Leu Val Ala Asp Gly Lys Phe Gly Thr Gln Glu Arg Val Asn
500 505 510
Asn Ser Asn Lys Lys Glu Trp Asn Gly Met Met Gly Glu Leu Leu Ser
515 520 525
Gly Gln Ala Asp Met Ile Val Ala Pro Leu Thr Ile Asn Asn Glu Arg
530 535 540
Ala Gln Tyr Ile Glu Phe Ser Lys Pro Phe Lys Tyr Gln Gly Leu Thr
545 550 555 560
Ile Leu Val Lys Lys Glu Ile Pro Arg Ser Thr Leu Asp Ser Phe Met
565 570 575
Gln Pro Phe Gln Ser Thr Leu Trp Leu Leu Val Gly Leu Ser Val His
580 585 590
Val Val Ala Val Met Leu Tyr Leu Leu Asp Arg Phe Ser Pro Phe Gly
595 600 605
Arg Phe Lys Val Asn Ser Glu Glu Glu Glu Asp Ala Leu Thr Leu
610 615 620
Ser Ser Ala Met Trp Phe Ser Trp Gly Val Leu Leu Asn Ser Gly Ile
625 630 635 640
Gly Glu Gly Ala Pro Arg Ser Phe Ser Ala Arg Ile Leu Gly Met Val
645 650 655
Trp Ala Gly Phe Ala Met Ile Ile Val Ala Ser Tyr Thr Ala Asn Leu

650	665	670
Ala		
Asn		
Asp		
Arg		
Pro		
Glu		
Glu		
Arg		
Ile		
Thr		
Gly		
Ile		
Leu		
Val		
Leu		
Asp		
Arg		
Pro		
Leu		
Arg		
Asn		
Pro		
Ser		
Asp		
Lys		
Phe		
Ile		
Tyr		
Ala		
Thr		
Met		
Tyr		
Arg		
His		
Met		
Glu		
Lys		
His		
Asn		
Tyr		
Asp		
Leu		
Glu		
Phe		
Glu		
Ala		
Ser		
Gln		
Lys		
Asn		
Val		
Leu		
Asp		
Arg		
Asn		
Lys		
Leu		
Asp		
Arg		
Asn		
Gln		
Lys		
Asn		
Gln		
Lys		
Asp		
Thr		
Val		
Leu		
Pro		
Arg		
Arg		
Ala		
Ile		
Glu		
Ala		
Gln		
Asn		
Gln		
Lys		
Asp		
Thr		
Val		
Leu		
Pro		
Arg		
Arg		
Ala		
Ile		
Glu		
Leu		
Gln		
Leu		
Cys		
Ser		
Arg		
His		
Arg		
Glu		
Ser		

(2) INFORMATION FOR SEQ ID NO:25:

- 'i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4157 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: both

- (ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 262..2937

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

CAAGCCGGGC GTTCGGAGCT GTGCCCGGCC CCGCTTCAGC ACCGCGGACA GCGCGGGCCG	60
CGTGGGGCTG AGCGCCGAGC CCCCCGCGCAC GCTTCAGCCC CCCTTCCCTC GGCGGACGTC	120
CCGGGACCGC CGCTCCGGGG GAGACGTGGC GTCCGCAGCC CGCGGGGCCG GGCGAGCGCA	180
GGACGGCCCG GAAGCCCCGC GGGGGATGCG CCGAGGGCCC CGCGTTCGCG CGCGCGAGAG	240
CCAGGGCCGC GGCCCGAGCC C ATG AGC ACC ATG CGC CTG CTG ACG CTC GCC Met Ser Thr Met Arg Leu Leu Thr Leu Ala	291
1 5 10	
CTG CTG TTC TCC TCC GTC GCC CGT GCC GCG TGC GAC CCC AAG ATC Leu Leu Phe Ser Cys Ser Val Ala Arg Ala Ala Cys Asp Pro Lys Ile	339
15 20 25	
GTC AAC ATT GGC GCG GTG CTG AGC ACG CGG AAG CAC GAG CAG ATG TTC Val Asn Ile Gly Ala Val Leu Ser Thr Arg Lys His Glu Gln Met Phe	387
30 35 40	
CGC GAG GCC GTG AAC CAG GCC AAC AAG CGG CAC GGC TCC TGG AAG ATT Arg Glu Ala Val Asn Gln Ala Asn Lys Arg His Gly Ser Trp Lys Ile	435
45 50 55	
CAG CTC AAT GCC ACC TCC GTC ACG CAC AAG CCC AAC GCC ATC CAG ATG Gln Leu Asn Ala Thr Ser Val Thr His Lys Pro Asn Ala Ile Gln Met	483
60 65 70	
GCT CTG TCG GTG TGC GAG GAC CTC ATC TCC AGC CAG GTC TAG GCG ATC Ala Leu Ser Val Cys Glu Asp Leu Ile Ser Ser Gln Val Tyr Ala Ile	531
75 80 85 90	
CTA GTT AGC CAT CCA CCT ACC CCC AAC GAC CAC TTC ACT CCC ACC CCT Leu Val Ser His Pro Pro Thr Pro Asn Asp His Phe Thr Pro Thr Pro	579
95 100 105	
GTC TCC TAC ACA GCC GGC TTC TAC CGC ATA CCC GTG CTG GGG CTG ACC Val Ser Tyr Ala Gly Phe Tyr Arg Ile Pro Val Leu Gly Leu Thr	627
110 115 120	
ACC CGC ATG TCC ATC TAC TCG GAC AAG AGC ATC CAC CTG AGC TTC CTG Thr Arg Met Ser Ile Tyr Ser Asp Lys Ser Ile His Leu Ser Phe Leu	675
125 130 135	
CGC ACC GTG CCG CCC TAC TCC CAC CAG TCC AGC GTG TGG TTT GAG ATG Arg Thr Val Pro Pro Tyr Ser His Gln Ser Ser Val Trp Phe Glu Met	723
140 145 150	
ATG CGT GTC TAC AGC TGG AAC CAC ATC ATC CTG CTG GTC AGC GAC GAC Met Arg Val Tyr Ser Trp Asn His Ile Ile Leu Leu Val Ser Asp Asp	771
155 160 165 170	
CAC GAG GGC CGG GCG GCT CAG AAA CGC CTG GAG ACG CTG CTG GAG GAG His Glu Gly Arg Ala Ala Gln Lys Arg Leu Glu Thr Leu Leu Glu Glu	819
175 180 185	
CGT GAG TCC AAG AGT AAA AAA AGG AAC TAT GAA AAC CTC GAC CAA CTG Arg Glu Ser Lys Ser Lys Lys Arg Asn Tyr Glu Asn Leu Asp Gln Leu	867
190 195 200	

TCC TAT GAC AAC AAG CGC GGA CCC AAG GCA GAG AAG GTG CTG CAG TTT Ser Tyr Asp Asn Lys Arg Gly Pro Lys Ala Glu Lys Val Leu Gln Phe	915
205 210 215	
GAC CCA GGG ACC AAG AAC GTG ACG GCC CTG CTG ATG GAG GCG AAA GAG Asp Pro Gly Thr Lys Asn Val Thr Ala Leu Leu Met Glu Ala Lys Glu	963
220 225 230	
CTG GAG GCC CGG GTC ATC ATC CTT TCT GCC AGC GAG GAC GAT GCT GCC Leu Glu Ala Arg Val Ile Ile Leu Ser Ala Ser Glu Asp Asp Ala Ala	1011
235 240 245 250	
ACT GTA TAC CGC GCA GCC GCG ATG CTG AAC ATG ACG GGC AAC ACC AAC Thr Val Tyr Arg Ala Ala Ala Met Leu Asn Met Thr Gly Asn Thr Asn	1059
255 260 265	
ATC TGG AAG ACC GGG CCG CTC TTC AAG AGA GTG CTG ATG TCT TCC AAG Ile Trp Lys Thr Gly Pro Leu Phe Lys Arg Val Leu Met Ser Ser Lys	1107
270 275 280	
TAT GCG GAT GGG GTG ACT GGT CGC GTG GAG TTC AAT GAG GAT GGG GAC Tyr Ala Asp Gly Val Thr Gly Arg Val Glu Phe Asn Glu Asp Gly Asp	1155
285 290 295	
CGG AAG TTC GCC AAC TAC AGC ATC ATG AAC CTG CAG AAC CGC AAG CTG Arg Lys Phe Ala Asn Tyr Ser Ile Met Asn Leu Gln Asn Arg Lys Leu	1203
300 305 310	
GTG CAA GTG GGC ATC TAC AAT GGC ACC CAC GTC ATC CCT AAT GAC AGG Val Gln Val Gly Ile Tyr Asn Gly Thr His Val Ile Pro Asn Asp Arg	1251
315 320 325 330	
AAG ATC ATC TGG CCA GGC GGA GAG ACA GAG AAG CCT CGA GGG TAC CAG Lys Ile Ile Trp Pro Gly Gly Glu Thr Cys Lys Pro Arg Gly Tyr Gln	1299
335 340 345	
ATG TCC ACC AGA CTG AAG ATT GTG ACG ATC CAC CAG GAG CCC TTC GTG Met Ser Thr Arg Leu Lys Ile Val Thr Ile His Gln Glu Pro Phe Val	1347
350 355 360	
TAC GTC AAG CCC ACG CTG AGT GAT GGG ACA TGC AAG GAG GAG TTC ACA Tyr Val Lys Pro Thr Leu Ser Asp Gly Thr Cys Lys Glu Glu Phe Thr	1395
365 370 375	
GTC AAC GGC GAC CCA GTC AAG AAG GTG ATC TGC ACC GGG CCC AAC GAC Val Asn Gly Asp Pro Val Lys Lys Val Ile Cys Thr Gly Pro Asn Asp	1443
380 385 390	
ACG TCG CCG GGC AGC CCC CGC CAC ACG GTG CCT CAG TGT TGC TAC GGC Thr Ser Pro Gly Ser Pro Arg His Thr Val Pro Gln Cys Cys Tyr Gly	1491
395 400 405 410	
TTT TGC ATC GAC CTG CTC ATC AAG CTG GCA CGG ACC ATG AAC TTC ACC Phe Cys Ile Asp Leu Leu Ile Lys Leu Ala Arg Thr Met Asn Phe Thr	1539
415 420 425	
TAC GAG GTG CAC CTG GTG GCA GAT GGC AAG TTC GGC ACA CAG GAG CGG Tyr Glu Val His Leu Val Ala Asp Gly Lys Phe Gly Thr Gln Glu Arg	1587
430 435 440	
GTG AAC AAC AGC AAC AAG AAG GAG TGG AAT GGG ATG ATG GGC GAG CTG Val Asn Asn Ser Asn Lys Lys Glu Trp Asn Gly Met Met Gly Glu Leu	1635
445 450 455	
CTC AGC GGG CAG GCA GAC ATG ATC GTG GCG CCG CTA ACC ATA AAC AAC Leu Ser Gly Gln Ala Asp Met Ile Val Ala Pro Leu Thr Ile Asn Asn	1683
460 465 470	

GAG CGC GCG CAG TAC ATC GAG TTT TCC AAG CCC TTC AAG TAC CAG GGC Glu Arg Ala Gln Tyr Ile Glu Phe Ser Lys Pro Phe Lys Tyr Gln Gly 475 480 485 490	1731
CTG ACT ATT CTG GTC AAG AAG GAG ATT CCC CGG AGC ACG CTG GAC TCG Leu Thr Ile Leu Val Lys Lys Glu Ile Pro Arg Ser Thr Leu Asp Ser 495 500 505	1779
TTC ATG CAG CCG TTC CAG AGC ACA CTG TGG CTG CTG GTG GGG CTG TCG Phe Met Gln Pro Phe Gln Ser Thr Leu Trp Leu Leu Val Gly Leu Ser 510 515 520	1827
GTG CAC GTG GTG GCC GTG ATG CTG TAC CTG CTG GAC CGC TTC AGC CCC Val His Val Val Ala Val Met Leu Tyr Leu Leu Asp Arg Phe Ser Pro 525 530 535	1875
TTC GGC CGG TTC AAG GTG AAC AGC GAG GAG GAG GAG GAC GCA CTG Phe Gly Arg Phe Lys Val Asn Ser Glu Glu Glu Glu Asp Ala Leu 540 545 550	1923
ACC CTG TCC TCG GCC ATG TGG TTC TCC TGG GGC GTC CTG CTC AAC TCC Thr Leu Ser Ser Ala Met Trp Phe Ser Trp Gly Val Leu Leu Asn Ser 555 560 565 570	1971
GGC ATC GGG GAA GGC GCC CCC AGA AGC TTC TCA GCG CGC ATC CTG GGC Gly Ile Gly Glu Gly Ala Pro Arg Ser Phe Ser Ala Arg Ile Leu Gly 575 580 585	2019
ATG GTG TGG GCC GGC TTT GCC ATG ATC ATC GTG GCC TCC TAC ACC GCC Met Val Trp Ala Gly Phe Ala Met Ile Ile Val Ala Ser Tyr Thr Ala 590 595 600	2067
AAC CTG GCG GCC TTC CTG GTG CTG GAC CGG CCG GAG GAG CGC ATC ACG Asn Leu Ala Ala Phe Leu Val Leu Asp Arg Pro Glu Glu Arg Ile Thr 605 610 615	2115
GGC ATC AAC GAC CCT CGG CTG AGG AAC CCC TCG GAC AAG TTT ATC TAC Gly Ile Asn Asp Pro Arg Leu Arg Asn Pro Ser Asp Lys Phe Ile Tyr 620 625 630	2163
GCC ACG GTG AAG CAG AGC TCC GTG GAT ATC TAC TTC CGG CGC CAG GTG Ala Thr Val Lys Gln Ser Ser Val Asp Ile Tyr Phe Arg Arg Gln Val 635 640 645 650	2211
GAG CTG AGC ACC ATG TAC CGG CAT ATG GAG AAG CAC AAC TAC GAG AGT Glu Leu Ser Thr Met Tyr Arg His Met Glu Lys His Asn Tyr Glu Ser 655 660 665	2259
GCG GCG GAG GCC ATC CAG GCC GTG AGA GAC AAC AAG CTG CAT GCC TTC Ala Ala Glu Ala Ile Gln Ala Val Arg Asp Asn Lys Leu His Ala Phe 670 675 680	2307
ATC TGG GAC TCG GCG GTG CTG GAG TTC GAG GCC TCG CAG AAG TGC GAC Ile Trp Asp Ser Ala Val Leu Glu Phe Glu Ala Ser Gln Lys Cys Asp 685 690 695	2355
CTG GTG ACG ACT GGA GAG CTG TTT TTC CGC TCG GGC TTC GGC ATA GGC Leu Val Thr Thr Gly Glu Leu Phe Phe Arg Ser Gly Phe Gly Ile Gly 700 705 710	2403
ATG CGC AAA GAC AGC CCC TGG AAG CAG AAC GTC TCC CTG TCC ATC CTC Met Arg Lys Asp Ser Pro Trp Lys Gln Asn Val Ser Leu Ser Ile Leu 715 720 725 730	2451
AAG TCC CAC GAG AAT GGC TTC ATG GAA GAC CTG GAC AAG ACG TGG GTT Lys Ser His Glu Asn Gly Phe Met Glu Asp Leu Asp Lys Thr Trp Val 735 740 745	2499

CGG TAT CAG GAA TGT GAC TCG CGC AGC AAC GCC CCT GCG ACC CTT ACT Arg Tyr Gln Glu Cys Asp Ser Arg Ser Asn Ala Pro Ala Thr Leu Thr 750 755 760	2547
TTT GAG AAC ATG GCC GGG GTC TTC ATG CTG GTA GCT GGG GGC ATC GTG Phe Glu Asn Met Ala Gly Val Phe Met Leu Val Ala Gly Gly Ile Val 765 770 775	2595
GCC GGG ATC TTC CTG ATT TTC ATC GAG ATT GCC TAC AAG CGG CAC AAG Ala Gly Ile Phe Leu Ile Phe Ile Glu Ile Ala Tyr Lys Arg His Lys 780 785 790	2643
GAT GCT CGC CGG AAG CAG ATG CAG CTG GCC TTT GCC GCC GTT AAC GTG Asp Ala Arg Arg Lys Gln Met Gln Leu Ala Phe Ala Ala Val Asn Val 795 800 805 810	2691
TGG CGG AAG AAC CTG CAG GAT AGA AAG AGT GGT AGA GCA GAG CCT GAC Trp Arg Lys Asn Leu Gln Asp Arg Lys Ser Gly Arg Ala Glu Pro Asp 815 820 825	2739
CCT AAA AAG AAA GCC ACA TTT AGG GCT ATC ACC TCC ACC CTG GCT TCC Pro Lys Lys Ala Thr Phe Arg Ala Ile Thr Ser Thr Leu Ala Ser 830 835 840	2787
AGC TTC AAG AGG CGT AGG TCC TCC AAA GAC ACG AGC ACC GGG GGT GGA Ser Phe Lys Arg Arg Ser Ser Lys Asp Thr Ser Thr Gly Gly Gly 845 850 855	2835
CGC GGT GCT TTG CAA AAC CAA AAA GAC ACA GTG CTG CCG CGA CGC GCT Arg Gly Ala Leu Gln Asn Gln Lys Asp Thr Val Leu Pro Arg Arg Ala 860 865 870	2883
ATT GAG AGG GAG GAG GGC CAG CTG CAG CTG TGT TCC CGT CAT AGG GAG Ile Glu Arg Glu Glu Gly Gln Leu Gln Leu Cys Ser Arg His Arg Glu 875 880 885 890	2931
AGC TGAGACTCCC CGCCCGCCCT CCTCTGCCCT CTCCCCCGCA GACAGACAGA Ser	2984
CAGACGGACG GGACAGCGGC CGGGCCCACG CAGAGCCCCG GAGCACACG GGGTCGGGG 3044	
AGGAGCACCC CCAGCCTCCC CCAGGCTGCG CCTGCCGCC CGCCGGTTGG CCGCTGGCC 3104	
GGTCCACCCC GTCCCGGCC CGCGCGTGCC CCCAGCGTGG GGCTAACGGG CGCCTTGTCT 3164	
GTGTATTTCT ATTTTGAGC AGTACCATCC CACTGATATC ACGGGCCCGC TCAACCTCTC 3224	
AGATCCCTCG GTCAGCACCG TGGTGTGAGG CCCCCGGAGG CGCCCACCTG CCCAGTTAGC 3284	
CGGGCCAAGG ACACTGATGG GTCCTGCTGC TCGGGAAAGC CTGAGGGAAAG CCCACCGCC 3344	
CCAGAGACTG CCCACCCCTGG GCCTCCCGTC CGTCCGCCG CCCACCCCGC TGCCTGGCG 3404	
GCAGCCCCCTG CTGGACCAAG GTGCGGACCG GAGCGGCTGA GGACGGGGCA GAGCTGAGTC 3464	
GGCTGGGCAG GGCGCGAGGG CGCTCCGGCA GAGGCAGGCC CCTGGGGTCT CTGAGCAGTG 3524	
GGGAGGGGG GCTAACTGCG CCCAGGGCGA GGGGCTTGGA GCAGAGACGG CAGCCCCATC 3584	
CTTCCCCGAG CACCAGCCTG AGCCACAGTG GGGCCCCTGG CCCCAGCTGG CTGGTGGCC 3644	
CCTCCTCGGG CGCCTGCGCT CCTCTGCAGC CTGAGCTCCA CCCTCCCTC TTCTTGGCG 3704	
ACCGCCCCACG AAACACCCCG TCTGCCCTT GACGCCACAC GCCGGGGCTG GCGCTGCCCT 3764	
CCCCCACGGC CGTCCCTGAC TTCCCCAGCTG GCAGCGCCTC CGGCCGCCCTC GGGCCGCCCTC 3824	

CTCCAGAATC GAGAGGGCTG AGCCCCTCCT CTCCTCGTCC GGCTGCAGC ACAGAAGGG	3884
GCCTCCCCGG GGGTCCCCGG AGCTGGCTC GGGACTGTCT TCAACCCCTGC CCTGCACCTT	3944
GGGCACGGGA GAGCGCCACC CGGCCGCCCC CGCCCTCGCT CGGGGTGCGT GACCGGCCCG	4004
CCACCTTGTA CAGAACCAAGG ACTCCCAGGG CCCGAGCGCG TGCCCTCCCC GTGCGCAGCC	4064
GCGCTCTGCC CCTCCGTCCC CAGGGTGCAG GCGCGCACCG CCCAACCCCC ACCTCCCGGT	4124
GTATGCAGTG GTGATGCCTA AAGGAATGTC ACG	4157

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 891 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Met Ser Thr Met Arg Leu Leu Thr Leu Ala Leu Leu Phe Ser Cys Ser	
1 5 10 15	
Val Ala Arg Ala Ala Cys Asp Pro Lys Ile Val Asn Ile Gly Ala Val	
20 25 30	
Leu Ser Thr Arg Lys His Glu Gln Met Phe Arg Glu Ala Val Asn Gln	
35 40 45	
Ala Asn Lys Arg His Gly Ser Trp Lys Ile Gln Leu Asn Ala Thr Ser	
50 55 60	
Val Thr His Lys Pro Asn Ala Ile Gln Met Ala Leu Ser Val Cys Glu	
65 70 75 80	
Asp Leu Ile Ser Ser Gln Val Tyr Ala Ile Leu Val Ser His Pro Pro	
85 90 95	
Thr Pro Asn Asp His Phe Thr Pro Thr Pro Val Ser Tyr Thr Ala Gly	
100 105 110	
Phe Tyr Arg Ile Pro Val Leu Gly Leu Thr Thr Arg Met Ser Ile Tyr	
115 120 125	
Ser Asp Lys Ser Ile His Leu Ser Phe Leu Arg Thr Val Pro Pro Tyr	
130 135 140	
Ser His Gln Ser Ser Val Trp Phe Glu Met Met Arg Val Tyr Ser Trp	
145 150 155 160	
Asn His Ile Ile Leu Leu Val Ser Asp Asp His Glu Gly Arg Ala Ala	
165 170 175	
Gln Lys Arg Leu Glu Thr Leu Leu Glu Glu Arg Glu Ser Lys Ser Lys	
180 185 190	
Lys Arg Asn Tyr Glu Asn Leu Asp Gln Leu Ser Tyr Asp Asn Lys Arg	
195 200 205	
Gly Pro Lys Ala Glu Lys Val Leu Gln Phe Asp Pro Gly Thr Lys Asn	
210 215 220	
Val Thr Ala Leu Leu Met Glu Ala Lys Glu Leu Glu Ala Arg Val Ile	

225	230	235	240
Ile Leu Ser Ala Ser Glu Asp Asp Ala Ala Thr Val Tyr Arg Ala Ala			
245	250	255	
Ala Met Leu Asn Met Thr Gly Asn Thr Asn Ile Trp Lys Thr Gly Pro			
260	265	270	
Leu Phe Lys Arg Val Leu Met Ser Ser Lys Tyr Ala Asp Gly Val Thr			
275	280	285	
Gly Arg Val Glu Phe Asn Glu Asp Gly Asp Arg Lys Phe Ala Asn Tyr			
290	295	300	
Ser Ile Met Asn Leu Gln Asn Arg Lys Leu Val Gln Val Gly Ile Tyr			
305	310	315	320
Asn Gly Thr His Val Ile Pro Asn Asp Arg Lys Ile Ile Trp Pro Gly			
325	330	335	
Gly Glu Thr Glu Lys Pro Arg Gly Tyr Gln Met Ser Thr Arg Leu Lys			
340	345	350	
Ile Val Thr Ile His Gln Glu Pro Phe Val Tyr Val Lys Pro Thr Leu			
355	360	365	
Ser Asp Gly Thr Cys Lys Glu Glu Phe Thr Val Asn Gly Asp Pro Val			
370	375	380	
Lys Lys Val Ile Cys Thr Gly Pro Asn Asp Thr Ser Pro Gly Ser Pro			
385	390	395	400
Arg His Thr Val Pro Gln Cys Cys Tyr Gly Phe Cys Ile Asp Leu Leu			
405	410	415	
Ile Lys Leu Ala Arg Thr Met Asn Phe Thr Tyr Glu Val His Leu Val			
420	425	430	
Ala Asp Gly Lys Phe Gly Thr Gln Glu Arg Val Asn Asn Ser Asn Lys			
435	440	445	
Lys Glu Trp Asn Gly Met Met Gly Glu Leu Leu Ser Gly Gln Ala Asp			
450	455	460	
Met Ile Val Ala Pro Leu Thr Ile Asn Asn Glu Arg Ala Gln Tyr Ile			
465	470	475	480
Glu Phe Ser Lys Pro Phe Lys Tyr Gln Gly Leu Thr Ile Leu Val Lys			
485	490	495	
Lys Glu Ile Pro Arg Ser Thr Leu Asp Ser Phe Met Gln Pro Phe Gln			
500	505	510	
Ser Thr Leu Trp Leu Leu Val Gly Leu Ser Val His Val Val Ala Val			
515	520	525	
Met Leu Tyr Leu Leu Asp Arg Phe Ser Pro Phe Gly Arg Phe Lys Val			
530	535	540	
Asn Ser Glu Glu Glu Glu Asp Ala Leu Thr Leu Ser Ser Ala Met			
545	550	555	560
Trp Phe Ser Trp Gly Val Leu Leu Asn Ser Gly Ile Gly Glu Gly Ala			
565	570	575	
Pro Arg Ser Phe Ser Ala Arg Ile Leu Gly Met Val Trp Ala Gly Phe			

580	585	590
Ala Met Ile Ile Val Ala Ser Tyr Thr Ala Asn Leu Ala Ala Phe Leu		
595	600	605
Val Leu Asp Arg Pro Glu Glu Arg Ile Thr Gly Ile Asn Asp Pro Arg		
610	615	620
Leu Arg Asn Pro Ser Asp Lys Phe Ile Tyr Ala Thr Val Lys Gln Ser		
625	630	635
Ser Val Asp Ile Tyr Phe Arg Arg Gln Val Glu Leu Ser Thr Met Tyr		
645	650	655
Arg His Met Glu Lys His Asn Tyr Glu Ser Ala Ala Glu Ala Ile Gln		
660	665	670
Ala Val Arg Asp Asn Lys Leu His Ala Phe Trp Asp Ser Ala Val		
675	680	685
Leu Glu Phe Glu Ala Ser Gln Lys Cys Asp Leu Val Thr Thr Gly Glu		
690	695	700
Leu Phe Phe Arg Ser Gly Phe Gly Ile Gly Met Arg Lys Asp Ser Pro		
705	710	715
720		
Trp Lys Gln Asn Val Ser Leu Ser Ile Leu Lys Ser His Glu Asn Gly		
725	730	735
Phe Met Glu Asp Leu Asp Lys Thr Trp Val Arg Tyr Gln Glu Cys Asp		
740	745	750
Ser Arg Ser Asn Ala Pro Ala Thr Leu Thr Phe Glu Asn Met Ala Gly		
755	760	765
Val Phe Met Leu Val Ala Gly Gly Ile Val Ala Gly Ile Phe Leu Ile		
770	775	780
Phe Ile Glu Ile Ala Tyr Lys Arg His Lys Asp Ala Arg Arg Lys Gln		
785	790	795
800		
Met Gln Leu Ala Phe Ala Ala Val Asn Val Trp Arg Lys Asn Leu Gln		
805	810	815
Asp Arg Lys Ser Gly Arg Ala Glu Pro Asp Pro Lys Lys Ala Thr		
820	825	830
Phe Arg Ala Ile Thr Ser Thr Leu Ala Ser Ser Phe Lys Arg Arg Arg		
835	840	845
Ser Ser Lys Asp Thr Ser Thr Gly Gly Arg Gly Ala Leu Gln Asn		
850	855	860
Gln Lys Asp Thr Val Leu Pro Arg Arg Ala Ile Glu Arg Glu Glu Gly		
865	870	875
880		
Gln Leu Gln Leu Cys Ser Arg His Arg Glu Ser		
885	890	

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 3794 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both

2) TOPOLOGY: both

MOLECULE TYPE: cDNA

(1x) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 262..2889

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

CAAGCCGGGC	GTCGGAGCT	GTGCCGGCC	CCGCTTCAGC	ACCGCGGACA	GCGCCGGCCG	60
CGTGGGGCTG	AGCGCCGAGC	CCCCGCGCAC	GCTTCAGCCC	CCCTTCCCTC	GGCCGACGTC	120
CCGGGACCGC	CGCTCCGGGG	GAGACGTGGC	GTCCGCAGCC	CGCGGGGCCG	GGCGAGCGCA	180
GGACGSCCCG	GAAGCCCCGC	GGGGGATGCG	CCGAGGGCCC	CGCGTTCGCG	CCGCGCAGAG	240
CCAGGCCCGC	GGCCCGAGCC	C ATG AGC ACC ATG CGC	CTG CTG ACG CTC	GCC		291
		Met Ser Thr Met Arg	Leu Leu Thr Leu Ala			
		1	5	10		
CTG CTG TTC TCC TGC TCC GTC	GCC CGT GCG	TGC GAC CCC AAG ATC				339
Leu Leu Phe Ser Cys Ser Val	Ala Arg Ala Ala	Cys Asp Pro Lys Ile				
15	20	25				
GTC AAC ATT GGC GCG GTG CTG AGC ACG CGG AAG CAC GAG CAG ATG TTC						387
Val Asn Ile Gly Ala Val Leu Ser Thr Arg Lys His Glu Gln Met Phe						
30	35	40				
CGC GAG GCC GTG AAC CAG GCC AAC AAG CGG CAC GGC TCC TGG AAG ATT						435
Arg Glu Ala Val Asn Gln Ala Asn Lys Arg His Gly Ser Trp Lys Ile						
45	50	55				
CAG CTC AAT GCC ACC TCC GTC ACG CAC AAG CCC AAC GCC ATC CAG ATG						483
Gln Leu Asn Ala Thr Ser Val Thr His Lys Pro Asn Ala Ile Gln Met						
60	65	70				
GCT CTG TCG GTG TGC GAG GAC CTC ATC TCC AGC CAG GTC TAC GCC ATC						531
Ala Leu Ser Val Cys Glu Asp Leu Ile Ser Ser Gln Val Tyr Ala Ile						
75	80	85				
90						
CTA GTT AGC CAT CCA CCT ACC CCC AAC GAC CAC TTC ACT CCC ACC CCT						579
Leu Val Ser His Pro Pro Thr Pro Asn Asp His Phe Thr Pro Thr Pro						
95	100	105				
GTC TCC TAC ACA GCG GGC TTC TAC CGC ATA CCC GTG CTG GGG CTG ACC						627
Val Ser Tyr Thr Ala Gly Phe Tyr Arg Ile Pro Val Leu Gly Leu Thr						
110	115	120				
ACC CGC ATG TCC ATC TAC TCG GAC AAG AGC ATC CAC CTG AGC TTC CTG						675
Thr Arg Met Ser Ile Tyr Ser Asp Lys Ser Ile His Leu Ser Phe Leu						
125	130	135				
CGC ACC GTG CCG CCC TAC TCC CAC CAG TCC AGC GTG TGG TTT GAG ATG						723
Arg Thr Val Pro Pro Tyr Ser His Gln Ser Ser Val Trp Phe Glu Met						
140	145	150				
ATG CGT GTC TAC AGC TGG AAC CAC ATC ATC CTG CTG GTC AGC GAC GAC						771
Met Arg Val Tyr Ser Trp Asn His Ile Ile Leu Leu Val Ser Asp Asp						
155	160	165				
170						
CAC GAG GGC CGG GCG GCT CAG AAA CGC CTG GAG ACG CTG CTG GAG GAG						819

His Glu Gly Arg Ala Ala Gln Lys Arg Leu Glu Thr Leu Leu Glu Glu	175	180	185	
CGT GAG TCC AAG AGT AAA AAA AGG AAC TAT GAA AAC CTC GAC CAA CTG				867
Arg Glu Ser Lys Ser Lys Lys Arg Asn Tyr Glu Asn Leu Asp Gln Leu	190	195	200	
TCC TAT GAC AAC AAG CGC GGA CCC AAG GCA GAG AAG GTG CTG CAG TTT				915
Ser Tyr Asp Asn Lys Arg Gly Pro Lys Ala Glu Lys Val Leu Gln Phe	205	210	215	
GAC CCA GGG ACC AAG AAC GTG ACG GCC CTG CTG ATG GAG GCG AAA GAG				963
Asp Pro Gly Thr Lys Asn Val Thr Ala Leu Leu Met Glu Ala Lys Glu	220	225	230	
CTG GAG GCC CGG GTC ATC ATC CTT TCT GCC AGC GAG GAC GAT GCT GCC				1011
Leu Glu Ala Arg Val Ile Ile Leu Ser Ala Ser Glu Asp Asp Ala Ala	235	240	245	250
ACT GTA TAC CGC GCA GCC GCG ATG CTG AAC ATG ACG GGC AAC ACC AAC				1059
Thr Val Tyr Arg Ala Ala Ala Met Leu Asn Met Thr Gly Asn Thr Asn	255	260	265	
ATC TGG AAG ACC GGG CCG CTC TTC AAG AGA GTG CTG ATG TCT TCC AAG				1107
Ile Trp Lys Thr Gly Pro Leu Phe Lys Arg Val Leu Met Ser Ser Lys	270	275	280	
TAT GCG GAT GGG GTG ACT GGT CGC GTG GAG TTC AAT GAG GAT GGG GAC				1155
Tyr Ala Asp Gly Val Thr Gly Arg Val Glu Phe Asn Glu Asp Gly Asp	285	290	295	
CGG AAG TTC GCC AAC TAC AGC ATC ATG AAC CTG CAG AAC CGC AAG CTG				1203
Arg Lys Phe Ala Asn Tyr Ser Ile Met Asn Leu Gln Asn Arg Lys Leu	300	305	310	
GTG CAA GTG GGC ATC TAC AAT GGC ACC CAC GTC ATC CCT AAT GAC AGG				1251
Val Gln Val Gly Ile Tyr Asn Gly Thr His Val Ile Pro Asn Asp Arg	315	320	325	330
AAG ATC ATC TGG CCA GGC GGA GAG ACA GAG AAG CCT CGA GGG TAC CAG				1299
Lys Ile Ile Trp Pro Gly Gly Glu Thr Glu Lys Pro Arg Gly Tyr Gln	335	340	345	
ATG TCC ACC AGA CTG AAG ATT GTG ACG ATC CAC CAG GAG CCC TTC GTG				1347
Met Ser Thr Arg Leu Lys Ile Val Thr Ile His Gln Glu Pro Phe Val	350	355	360	
TAC GTC AAG CCC ACG CTG AGT GAT GGG ACA TGC AAG GAG GAG TTC ACA				1395
Tyr Val Lys Pro Thr Leu Ser Asp Gly Thr Cys Lys Glu Glu Phe Thr	365	370	375	
GTC AAC GGC GAC CCA GTC AAG AAG GTG ATC TGC ACC GGG CCC AAC GAC				1443
Val Asn Gly Asp Pro Val Lys Lys Val Ile Cys Thr Gly Pro Asn Asp	380	385	390	
ACG TCG CCG GGC AGC CCC CGC CAC ACG GTG CCT CAG TGT TGC TAC GGC				1491
Thr Ser Pro Gly Ser Pro Arg His Thr Val Pro Gln Cys Cys Tyr Gly	395	400	405	410
TTT TGC ATC GAC CTG CTC ATC AAG CTG GCA CGG ACC ATG AAC TTC ACC				1539
Phe Cys Ile Asp Leu Leu Ile Lys Leu Ala Arg Thr Met Asn Phe Thr	415	420	425	
TAC GAG GTG CAC CTG GTG GCA GAT GGC AAG TTC GGC ACA CAG GAG CGG				1587
Tyr Glu Val His Leu Val Ala Asp Gly Lys Phe Gly Thr Gln Glu Arg	430	435	440	

GTG AAC AAC AGC AAC AAG GAG TGG AAT GGG ATG ATG GGC GAG CTG Val Asn Asn Ser Asn Lys Lys Glu Trp Asn ...y Met Met Gly Glu Leu 445 450 455	1635
CTC AGC GGG CAG GCA GAC ATG ATC GTG GCG CCG CTA ACC ATA AAC AAC Leu Ser Gly Gln Ala Asp Met Ile Val Ala Pro Leu Thr Ile Asn Asn 460 465 470	1683
GAG CGC GCG CAG TAC ATC GAG TTT TCC AAG CCC TTC AAG TAC CAG GGC Glu Arg Ala Gln Tyr Ile Glu Phe Ser Lys Pro Phe Lys Tyr Gln Gly 475 480 485 490	1731
CTG ACT ATT CTG GTC AAG AAG GAG ATT CCC CCG AGC ACG CTG GAC TCG Leu Thr Ile Leu Val Lys Glu Ile Pro Arg Ser Thr Leu Asp Ser 495 500 505	1779
TTC ATG CAG CCG TTC CAG AGC ACA CTG TGG CTG CTG GTG GGG CTG TCG Phe Met Gln Pro Phe Gln Ser Thr Leu Trp Leu Leu Val Gly Leu Ser 510 515 520	1827
GTG CAC GTG GTG GCC GTG ATG CTG TAC CTG CTG GAC CGC TTC AGC CCC Val His Val Val Ala Val Met Leu Tyr Leu Leu Asp Arg Phe Ser Pro 525 530 535	1875
TTC GGC CGG TTC AAG GTG AAC AGC GAG GAG GAG GAG GAC GCA CTG Phe Gly Arg Phe Lys Val Asn Ser Glu Glu Glu Glu Asp Ala Leu 540 545 550	1923
ACC CTG TCC TCG GCC ATG TGG TTC TCC TGG GGC GTC CTG CTC AAC TCC Thr Leu Ser Ser Ala Met Trp Phe Ser Trp Gly Val Leu Leu Asn Ser 555 560 565 570	1971
GGC ATC GGG GAA GGC GCC CCC AGA AGC TTC TCA GCG CGC ATC CTG GGC Gly Ile Gly Glu Gly Ala Pro Arg Ser Phe Ser Ala Arg Ile Leu Gly 575 580 585	2019
ATG GTG TGG GCC GGC TTT GCC ATG ATC ATC GTG GCC TCC TAC ACC GCC Met Val Trp Ala Gly Phe Ala Met Ile Ile Val Ala Ser Tyr Thr Ala 590 595 600	2067
AAC CTG GCG GCC TTC CTG GTG CTG GAC CGG CCG GAG GAG CGC ATC ACG Asn Leu Ala Ala Phe Leu Val Leu Asp Arg Pro Glu Glu Arg Ile Thr 605 610 615	2115
GGC ATC AAC GAC CCT CGG CTG AGG AAC CCC TCG GAC AAG TTT ATC TAC Gly Ile Asn Asp Pro Arg Leu Arg Asn Pro Ser Asp Lys Phe Ile Tyr 620 625 630	2163
GCC ACG GTG AAG CAG AGC TCC GTG GAT ATC TAC TTC CGG CGC CAG GTG Ala Thr Val Lys Gln Ser Ser Val Asp Ile Tyr Phe Arg Arg Gln Val 635 640 645 650	2211
GAG CTG AGC ACC ATG TAC CGG CAT ATG GAG AAG CAC AAC TAC GAG AGT Glu Leu Ser Thr Met Tyr Arg His Met Glu Lys His Asn Tyr Glu Ser 655 660 665	2259
GCG GCG GAG GCC ATC CAG GCC GTG AGA GAC AAC AAG CTG CAT GCC TTC Ala Ala Glu Ala Ile Gln Ala Val Arg Asp Asn Lys Leu His Ala Phe 670 675 680	2307
ATC TGG GAC TCG GCG GTG CTG GAG TTC GAG GCC TCG CAG AAG TGC GAC Ile Trp Asp Ser Ala Val Leu Glu Phe Glu Ala Ser Gln Lys Cys Asp 685 690 695	2355
CTG GTG ACG ACT GGA GAG CTG TTT TTC CGC TCG GGC TTC GGC ATA GGC Leu Val Thr Thr Gly Glu Leu Phe Phe Arg Ser Gly Phe Gly Ile Gly 700 705 710	2403

ATG CGC AAA GAC AGC CCC TGG AAG CAG AAC GTC TCC CTG TCC ATC CTC Met Arg Lys Asp Ser Pro Trp Lys Gln Asn Val Ser Leu Ser Ile Leu 715 720 725 730	2451
AAG TCC CAC GAG AAT GGC TTC ATG GAA GAC CTG GAC AAG ACG TGG GTT Lys Ser His Glu Asn Gly Phe Met Glu Asp Leu Asp Lys Thr Trp Val 735 740 745	2499
CGG TAT CAG GAA TGT GAC TCG CGC AGC AAC GCC CCT GCG ACC CTT ACT Arg Tyr Gln Glu Cys Asp Ser Arg Ser Asn Ala Pro Ala Thr Leu Thr 750 755 760	2547
TTT GAG AAC ATG GCC GGG GTC TTC ATG CTG GTA GCT GGG GGC ATC GTG Phe Glu Asn Met Ala Gly Val Phe Met Leu Val Ala Gly Gly Ile Val 765 770 775	2595
GCC GGG ATC TTC CTG ATT TTC ATC GAG ATT GCC TAC AAG CGG CAC AAG Ala Gly Ile Phe Leu Ile Phe Ile Glu Ile Ala Tyr Lys Arg His Lys 780 785 790	2643
GAT GCT CGC CGG AAG CAG ATG CAG CTG GCC TTT GCC GCC GTT AAC GTG Asp Ala Arg Arg Lys Gln Met Gln Leu Ala Phe Ala Ala Val Asn Val 795 800 805 810	2691
TGG CGG AAG AAC CTG CAG GAT AGA AAG AGT GGT AGA GCA GAG CCT GAC Trp Arg Lys Asn Leu Gln Asp Arg Lys Ser Gly Arg Ala Glu Pro Asp 815 820 825	2739
CCT AAA AAG AAA GCC ACA TTT AGG GCT ATC ACC TCC ACC CTG GCT TCC Pro Lys Lys Ala Thr Phe Arg Ala Ile Thr Ser Thr Leu Ala Ser 830 835 840	2787
AGC TTC AAG AGG CGT AGG TCC TCC AAA GAC ACG CAG TAC CAT CCC ACT Ser Phe Lys Arg Arg Ser Ser Lys Asp Thr Gln Tyr His Pro Thr 845 850 855	2835
GAT ATC ACG GGC CCG CTC AAC CTC TCA GAT CCC TCG GTC AGC ACC GTG Asp Ile Thr Gly Pro Leu Asn Leu Ser Asp Pro Ser Val Ser Thr Val 860 865 870	2883
GTG TGAGGCCCGG GGAGGCGCCC ACCTGCCAG TTAGCCGGC CAAGGACACT Val 875	2936
GATGGGTCT GCTGCTCGGG AAGGCCTGAG GGAAGCCCAC CCGCCCCAGA GACTGCCAC	2996
CCTGGGCCTC CCGTCCGTCC GCCCCCCCAC CCCGCTGCCT GGCGGGCAGC CCCTGCTGGA	3056
CCAAAGGTGCG GACCGGAGCG GCTGAGGACG GGGCAGAGCT GAGTCGGCTG GGCAGGGCCG	3116
CAGGGCGCTC CGGCAGAGGC AGGCCCTGG GGTCTCTGAG CAGTGGGAG CGGGGGCTAA	3176
CTGCCCCCAG GCGGAGGGGC TTGGAGCAGA GACGGCAGCC CCATCCTTCC CGCAGCACCA	3236
GCCTGAGCCA CAGTGGGGCC CATGGCCCCA GCTGGCTGGG TCAGCCCCCTCC TCAGGGCGCT	3296
GCGCTCCTCT GCAGCCTGAG CTCCACCCCTC CCCTCTTCTT GCGGCACCGC CCACCAAACA	3356
CCCCGCTCTGC CCCTTGACGC CACACGCCGG GGCTGGCGCT GCCCTCCCCC ACGGCGGTCC	3416
CTGACTTCCC AGCTGGCAGC GCCTCCCGCC GCCTCGGGCC GCCTCCTCCA GAATCGAGAG	3476
GGCTGAGCC CTCTCTCTCT CGTCCGGCCT GCAGCACAGA AGGGGGCCTC CCCGGGGGTC	3536
CCCGGACGCT GGCTCGGGAC TGTCTAAC CCTGCCCTGC ACCTTGGGCA CGGGAGAGCG	3596
CCACCCGCCG GCCCCCGCCC TCGCTCCGGG TGCCTGACCG GCGCGCCACC TTGTACAGAA	3656

CCAGCACTCC CAGGGCCCCGA GCGCGTGCCT TCCCCGTGCG CAGCCGCGCT CTGCCCTCC	3716
GTCCCCAGGG TGCAGGCACG CACCGCCCAA CCCCCACCTC CCGGTGTATG CAGTGGTGAT	3776
GCCTAAAGGA ATGTCACG	3794

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 875 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Met Ser Thr Met Arg Leu Leu Thr Leu Ala Leu Leu Phe Ser Cys Ser	
1 5 10 15	
Val Ala Arg Ala Ala Cys Asp Pro Lys Ile Val Asn Ile Gly Ala Val	
20 25 30	
Leu Ser Thr Arg Lys His Glu Gln Met Phe Arg Glu Ala Val Asn Gln	
35 40 45	
Ala Asn Lys Arg His Gly Ser Trp Lys Ile Gln Leu Asn Ala Thr Ser	
50 55 60	
Val Thr His Lys Pro Asn Ala Ile Gln Met Ala Leu Ser Val Cys Glu	
65 70 75 80	
Asp Leu Ile Ser Ser Gln Val Tyr Ala Ile Leu Val Ser His Pro Pro	
85 90 95	
Thr Pro Asn Asp His Phe Thr Pro Thr Pro Val Ser Tyr Thr Ala Gly	
100 105 110	
Phe Tyr Arg Ile Pro Val Leu Gly Leu Thr Thr Arg Met Ser Ile Tyr	
115 120 125	
Ser Asp Lys Ser Ile His Leu Ser Phe Leu Arg Thr Val Pro Pro Tyr	
130 135 140	
Ser His Gln Ser Ser Val Trp Phe Glu Met Met Arg Val Tyr Ser Trp	
145 150 155 160	
Asn His Ile Ile Leu Leu Val Ser Asp Asp His Glu Gly Arg Ala Ala	
165 170 175	
Gln Lys Arg Leu Glu Thr Leu Leu Glu Arg Glu Ser Lys Ser Lys	
180 185 190	
Lys Arg Asn Tyr Glu Asn Leu Asp Gln Leu Ser Tyr Asp Asn Lys Arg	
195 200 205	
Gly Pro Lys Ala Glu Lys Val Leu Gln Phe Asp Pro Gly Thr Lys Asn	
210 215 220	
Val Thr Ala Leu Leu Met Glu Ala Lys Glu Leu Glu Ala Arg Val Ile	
225 230 235 240	
Ile Leu Ser Ala Ser Glu Asp Asp Ala Ala Thr Val Tyr Arg Ala Ala	
245 250 255	
Ala Met Leu Asn Met Thr Gly Asn Thr Asn Ile Trp Lys Thr Gly Pro	

260

265

270

Leu Phe Lys Arg Val Leu Met Ser Ser Lys Tyr Ala Asp Gly Val Thr
275 280 285

Gly Arg Val Glu Phe Asn Glu Asp Gly Asp Arg Lys Phe Ala Asn Tyr
290 295 300

Ser Ile Met Asn Leu Gln Asn Arg Lys Leu Val Gln Val Gly Ile Tyr
305 310 315 320

Asn Gly Thr His Val Ile Pro Asn Asp Arg Lys Ile Ile Trp Pro Gly
325 330 335

Gly Glu Thr Glu Lys Pro Arg Gly Tyr Gln Met Ser Thr Arg Leu Lys
340 345 350

Ile Val Thr Ile His Gln Glu Pro Phe Val Tyr Val Lys Pro Thr Leu
355 360 365

Ser Asp Gly Thr Cys Lys Glu Glu Phe Thr Val Asn Gly Asp Pro Val
370 375 380

Lys Lys Val Ile Cys Thr Gly Pro Asn Asp Thr Ser Pro Gly Ser Pro
385 390 395 400

Arg His Thr Val Pro Gln Cys Cys Tyr Gly Phe Cys Ile Asp Leu Leu
405 410 415

Ile Lys Leu Ala Arg Thr Met Asn Phe Thr Tyr Glu Val His Leu Val
420 425 430

Ala Asp Gly Lys Phe Gly Thr Gln Glu Arg Val Asn Ser Asn Lys
435 440 445

Lys Glu Trp Asn Gly Met Met Gly Glu Leu Leu Ser Gly Gln Ala Asp
450 455 460

Met Ile Val Ala Pro Leu Thr Ile Asn Asn Glu Arg Ala Gln Tyr Ile
465 470 475 480

Glu Phe Ser Lys Pro Phe Lys Tyr Gln Gly Leu Thr Ile Leu Val Lys
485 490 495

Lys Glu Ile Pro Arg Ser Thr Leu Asp Ser Phe Met Gln Pro Phe Gln
500 505 510

Ser Thr Leu Trp Leu Leu Val Gly Leu Ser Val His Val Val Ala Val
515 520 525

Met Leu Tyr Leu Leu Asp Arg Phe Ser Pro Phe Gly Arg Phe Lys Val
530 535 540

Asn Ser Glu Glu Glu Glu Asp Ala Leu Thr Leu Ser Ser Ala Met
545 550 555 560

Trp Phe Ser Trp Gly Val Leu Leu Asn Ser Gly Ile Gly Glu Gly Ala
565 570 575

Pro Arg Ser Phe Ser Ala Arg Ile Leu Gly Met Val Trp Ala Gly Phe
580 585 590

Ala Met Ile Ile Val Ala Ser Tyr Thr Ala Asn Leu Ala Ala Phe Leu
595 600 605

Val Leu Asp Arg Pro Glu Glu Arg Ile Thr Gly Ile Asn Asp Pro Arg
610 615 620

Leu Arg Asn Pro Ser Asp Lys Phe Ile Tyr Ala Thr Val Lys Gln Ser
625 630 635 640

Ser Val Asp Ile Tyr Phe Arg Arg Gln Val Glu Leu Ser Thr Met Tyr
645 650 655

Arg His Met Glu Lys His Asn Tyr Glu Ser Ala Ala Glu Ala Ile Gln
660 665 670

Ala Val Arg Asp Asn Lys Leu His Ala Phe Ile Trp Asp Ser Ala Val
675 680 685

Leu Glu Phe Glu Ala Ser Gln Lys Cys Asp Leu Val Thr Thr Gly Glu
690 695 700

Leu Phe Phe Arg Ser Gly Phe Gly Ile Gly Met Arg Lys Asp Ser Pro
705 710 715 720

Trp Lys Gln Asn Val Ser Leu Ser Ile Leu Lys Ser His Glu Asn Gly
725 730 735

Phe Met Glu Asp Leu Asp Lys Thr Trp Val Arg Tyr Gln Glu Cys Asp
740 745 750

Ser Arg Ser Asn Ala Pro Ala Thr Leu Thr Phe Glu Asn Met Ala Gly
755 760 765

Val Phe Met Leu Val Ala Gly Gly Ile Val Ala Gly Ile Phe Leu Ile
770 775 780

Phe Ile Glu Ile Ala Tyr Lys Arg His Lys Asp Ala Arg Arg Lys Gln
785 790 795 800

Met Gln Leu Ala Phe Ala Ala Val Asn Val Trp Arg Lys Asn Leu Gln
805 810 815

Asp Arg Lys Ser Gly Arg Ala Glu Pro Asp Pro Lys Lys Ala Thr
820 825 830

Phe Arg Ala Ile Thr Ser Thr Leu Ala Ser Ser Phe Lys Arg Arg Arg
835 840 845

Ser Ser Lys Asp Thr Gln Tyr His Pro Thr Asp Ile Thr Gly Pro Leu
850 855 860

Asn Leu Ser Asp Pro Ser Val Ser Thr Val Val
865 870 875

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4094 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 262..2874

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

CAAGCCGGGC GTTCGGAGCT GTGCCGGCC CCGCTTCAGC ACCGCGGACA GCGCCGGCCG	60
CGTGGGGCTG AGCGCCGAGC CCCCCGGCAC GCCTCAGCCC CCCTTCCCTC GGCGGACGTC	120
CCGGGACCGC CGCTCCGGGG GAGACGTGGC GTCCGCAGCC CGCGGGGCCG GGCGAGCGCA	180
GGACGGCCCG GAAGCCCCGC GGGGGATGCG CCGAGGGCCC CGCGTTCGCG CGCGCAGAG	240
CCAGGCCCCGC GGCCCGAGCC C ATG AGC ACC ATG CGC CTG CTG ACG CTC GCC Met Ser Thr Met Arg Leu Leu Thr Leu Ala	291
1 5 10	
CTG CTG TTC TCC TGC TCC GTC GCC CGT GCC GCG TGC GAC CCC AAG ATC Leu Leu Phe Ser Cys Ser Val Ala Arg Ala Ala Cys Asp Pro Lys Ile	339
15 20 25	
GTC AAC ATT GGC GCG GTG CTG AGC ACG CGG AAG CAC GAG CAG ATG TTC Val Asn Ile Gly Ala Val Leu Ser Thr Arg Lys His Glu Gln Met Phe	387
30 35 40	
CGC GAG GCC GTG AAC CAG GCC AAC AAG CGG CAC GGC TCC TGG AAG ATT Arg Glu Ala Val Asn Gln Ala Asn Lys Arg His Gly Ser Trp Lys Ile	435
45 50 55	
CAG CTC AAT GCC ACC TCC GTC ACG CAC AAG CCC AAC GCC ATC CAG ATG Gln Leu Asn Ala Thr Ser Val Thr His Lys Pro Asn Ala Ile Gln Met	483
60 65 70	
GCT CTG TCG GTG TGC GAG GAC CTC ATC TCC AGC CAG GTC TAC GCC ATC Ala Leu Ser Val Cys Glu Asp Leu Ile Ser Ser Gln Val Tyr Ala Ile	531
75 80 85 90	
CTA GTT AGC CAT CCA CCT ACC CCC AAC GAC CAC TTC ACT CCC ACC CCT Leu Val Ser His Pro Pro Thr Pro Asn Asp His Phe Thr Pro Thr Pro	579
95 100 105	
GTC TCC TAC ACA GCC GGC TTC TAC CGC ATA CCC GTG CTG GGG CTG ACC Val Ser Tyr Thr Ala Gly Phe Tyr Arg Ile Pro Val Leu Gly Leu Thr	627
110 115 120	
ACC CGC ATG TCC ATC TAC TCG GAC AAG AGC ATC CAC CTG AGC TTC CTG Thr Arg Met Ser Ile Tyr Ser Asp Lys Ser Ile His Leu Ser Phe Leu	675
125 130 135	
CGC ACC GTG CCG CCC TAC TCC CAC CAG TCC AGC GTG TGG TTT GAG ATG Arg Thr Val Pro Pro Tyr Ser His Gln Ser Ser Val Trp Phe Glu Met	723
140 145 150	
ATG CGT GTC TAC AGC TGG AAC CAC ATC ATC CTG CTG GTC AGC GAC GAC Met Arg Val Tyr Ser Trp Asn His Ile Ile Leu Leu Val Ser Asp Asp	771
155 160 165 170	
CAC GAG GGC CGG GCG GCT CAG AAA CGC CTG GAG ACG CTG CTG GAG GAG His Glu Gly Arg Ala Ala Gln Lys Arg Leu Glu Thr Leu Leu Glu Glu	819
175 180 185	
CGT GAG TCC AAG GCA GAG AAG GTG CTG CAG TTT GAC CCA GGG ACC AAG Arg Glu Ser Lys Ala Glu Lys Val Leu Gln Phe Asp Pro Gly Thr Lys	867
190 195 200	
AAC GTG ACG GCC CTG CTG ATG GAG GCG AAA GAG CTG GAG GCC CGG GTC Asn Val Thr Ala Leu Leu Met Glu Ala Lys Glu Leu Glu Ala Arg Val	915
205 210 215	
ATC ATC CTT TCT GCC AGC GAG GAC GAT GCT GCC ACT GTA TAC CGC GCA Ile Ile Leu Ser Ala Ser Glu Asp Asp Ala Ala Thr Val Tyr Arg Ala	963
220 225 230	

GCC GCG ATG CTG AAC ATG ACC GGC AAC ACC AAC ATC TGG AAG ACC GGG Ala Ala Met Leu Asn Met Thr Gly Asn Thr Asn Ile Trp Lys Thr Gly 235 240 245 250	1011
CCG CTC TTC AAG AGA GTG CTG ATG TCT TCC AAG TAT GCG GAT GGG GTG Pro Leu Phe Lys Arg Val Leu Met Ser Ser Lys Tyr Ala Asp Gly Val 255 260 265	1059
ACT GGT CGC GTG GAG TTC AAT GAG GAT GGG GAC CGG AAG TTC GCC AAC Thr Gly Arg Val Glu Phe Asn Glu Asp Gly Asp Arg Lys Phe Ala Asn 270 275 280	1107
TAC AGC ATC ATG AAC CTG CAG AAC CGC AAG CTG GTG CAA GTG GGC ATC Tyr Ser Ile Met Asn Leu Gln Asn Arg Lys Leu Val Gln Val Gly Ile 285 290 295	1155
TAC AAT GGC ACC CAC GTC ATC CCT AAT GAC AGG AAG ATC ATC TGG CCA Tyr Asn Gly Thr His Val Ile Pro Asn Asp Arg Lys Ile Ile Trp Pro 300 305 310	1203
GGC GGA GAG ACA GAG AAG CCT CGA GGG TAC CAG ATG TCC ACC AGA CTG Gly Gly Glu Thr Glu Lys Pro Arg Gly Tyr Gln Met Ser Thr Arg Leu 315 320 325 330	1251
AAG ATT GTG ACG ATC CAC CAG GAG CCC TTC GTG TAC GTC AAG CCC ACG Lys Ile Val Thr Ile His Gln Glu Pro Phe Val Tyr Val Lys Pro Thr 335 340 345	1299
CTG AGT GAT GGG ACA TGC AAG GAG TTC ACA GTC AAC GGC GAC CCA Leu Ser Asp Gly Thr Cys Lys Glu Phe Thr Val Asn Gly Asp Pro 350 355 360	1347
GTC AAG AAG GTG ATC TGC ACC GGG CCC AAC GAC ACG TCG CCG GGC AGC Val Lys Val Ile Cys Thr Gly Pro Asn Asp Thr Ser Pro Gly Ser 365 370 375	1395
CCC CGC CAC ACG GTG CCT CAG TGT TGC TAC GGC TTT TGC ATC GAC CTG Pro Arg His Thr Val Pro Gln Cys Cys Tyr Gly Phe Cys Ile Asp Leu 380 385 390	1443
CTC ATC AAG CTG GCA CGG ACC ATG AAC TTC ACC TAC GAG GTG CAC CTG Leu Ile Lys Leu Ala Arg Thr Met Asn Phe Thr Tyr Glu Val His Leu 395 400 405 410	1491
GTG GCA GAT GGC AAG TTC GGC ACA CAG GAG CGG GTG AAC AAC AGC AAC Val Ala Asp Gly Lys Phe Gly Thr Gln Glu Arg Val Asn Asn Ser Asn 415 420 425	1539
AAG AAG GAG TGG AAT GGG ATG ATG GGC GAG CTG CTC AGC GGG CAG GCA Lys Lys Glu Trp Asn Gly Met Met Gly Glu Leu Leu Ser Gly Gln Ala 430 435 440	1587
GAC ATG ATC GTG GCG CCG CTA ACC ATA AAC AAC GAG CGC GCG CAG TAC Asp Met Ile Val Ala Pro Leu Thr Ile Asn Asn Glu Arg Ala Gln Tyr 445 450 455	1635
ATC GAG TTT TCC AAG CCC TTC AAG TAC CAG GGC CTG ACT ATT CTG GTC Ile Glu Phe Ser Lys Pro Phe Lys Tyr Gln Gly Leu Thr Ile Leu Val 460 465 470	1683
AAG AAG GAG ATT CCC CGG AGC ACG CTG GAC TCG TTC ATG CAG CCG TTC Lys Lys Glu Ile Pro Arg Ser Thr Leu Asp Ser Phe Met Gln Pro Phe 475 480 485 490	1731
CAG AGC ACA CTG TGG CTG CTG GTG GGG CTG TCG GTG CAC GTG GTG GCC Gln Ser Thr Leu Trp Leu Leu Val Gly Leu Ser Val His Val Val Ala	1779

495	500	505	
GTG ATG CTG TAC CTG CTG GAC CGC TTC AGC CCC TTC GGC CGG TTC AAG Val Met Leu Tyr Leu Leu Asp Arg Phe Ser Pro Phe Gly Arg Phe Lys 510	515	520	1827
GTG AAC AGC GAG GAG GAG GAG GAC GCA CTG ACC CTG TCC TCG GCC Val Asn Ser Glu Glu Glu Asp Ala Leu Thr Leu Ser Ser Ala 525	530	535	1875
ATG TGG TTC TCC TGG GGC GTC CTG CTC AAC TCC GGC ATC GGG GAA GGC Met Trp Phe Ser Trp Gly Val Leu Leu Asn Ser Gly Ile Gly Glu Gly 540	545	550	1923
GCC CCC AGA AGC TTC TCA GCG CGC ATC CTG GGC ATG GTG TGG GCC GGC Ala Pro Arg Ser Phe Ser Ala Arg Ile Leu Gly Met Val Trp Ala Gly 555	560	565	1971
TTT GCC ATG ATC ATC GTG GCC TCC TAC ACC GCC AAC CTG GCG GCC TTC Phe Ala Met Ile Ile Val Ala Ser Tyr Thr Ala Asn Leu Ala Ala Phe 575	580	585	2019
CTG GTG CTG GAC CGG CCG GAG GAG CGC ATC ACG GGC ATC AAC GAC CCT Leu Val Leu Asp Arg Pro Glu Glu Arg Ile Thr Gly Ile Asn Asp Pro 590	595	600	2067
CGG CTG AGG AAC CCC TCG GAC AAG TTT ATC TAC GCC ACG GTG AAG CAG Arg Leu Arg Asn Pro Ser Asp Lys Phe Ile Tyr Ala Thr Val Lys Gln 605	610	615	2115
AGC TCC GTG GAT ATC TAC TTC CGG CGC CAG GTG GAG CTG AGC ACC ATG Ser Ser Val Asp Ile Tyr Phe Arg Arg Gln Val Glu Leu Ser Thr Met 620	625	630	2163
TAC CGG CAT ATG GAG AAG CAC AAC TAC GAG AGT GCG GCG GAG GCC ATC Tyr Arg His Met Glu Lys His Asn Tyr Glu Ser Ala Ala Glu Ala Ile 635	640	645	2211
CAG GCC GTG AGA GAC AAC AAG CTG CAT GCC TTC ATC TGG GAC TCG GCG Gln Ala Val Arg Asp Asn Lys Leu His Ala Phe Ile Trp Asp Ser Ala 655	660	665	2259
GTG CTG GAG TTC GAG GCC TCG CAG AAG TGC GAC CTG GTG ACG ACT GGA Val Leu Glu Phe Glu Ala Ser Gln Lys Cys Asp Leu Val Thr Thr Gly 670	675	680	2307
GAG CTG TTT TTC CGC TCG GGC TTC GGC ATA GGC ATG CGC AAA GAC AGC Glu Leu Phe Phe Arg Ser Gly Phe Gly Ile Gly Met Arg Lys Asp Ser 685	690	695	2355
CCC TGG AAG CAG AAC GTC TCC CTG TCC ATC CTC AAG TCC CAC GAG AAT Pro Trp Lys Gln Asn Val Ser Leu Ser Ile Leu Lys Ser His Glu Asn 700	705	710	2403
GGC TTC ATG GAA GAC CTG GAC AAG ACG TGG GTT CGG TAT CAG GAA TGT Gly Phe Met Glu Asp Leu Asp Lys Thr Trp Val Arg Tyr Gln Glu Cys 715	720	725	2451
GAC TCG CGC AGC AAC GCC CCT GCG ACC CTT ACT TTT GAG AAC ATG GCC Asp Ser Arg Ser Asn Ala Pro Ala Thr Leu Thr Phe Glu Asn Met Ala 735	740	745	2499
GGG GTC TTC ATG CTG GTA GCT GGG GGC ATC GTG GCC GGG ATC TTC CTG Gly Val Phe Met Leu Val Ala Gly Gly Ile Val Ala Gly Ile Phe Leu 750	755	760	2547
ATT TTC ATC GAG ATT GCC TAC AAG CGG CAC AAG GAT GCT CGC CGG AAG			2595

Ile Phe Ile Glu Ile Ala Tyr Lys Arg His Lys Asp Ala Arg Arg Lys	765	770	775	
CAG ATG CAG CTG GCC TTT GCC GCT AAC GTG TGG CGG AAG AAC CTG				2643
Gln Met Gln Leu Ala Phe Ala Ala Val Asn Val Trp Arg Lys Asn Leu				
780	785	790		
CAG GAT AGA AAG AGT GGT AGA GCA GAG CCT GAC CCT AAA AAG AAA GCC				2691
Gln Asp Arg Lys Ser Gly Arg Ala Glu Pro Asp Pro Lys Lys Ala				
795	800	805	810	
ACA TTT AGG GCT ATC ACC TCC ACC CTG GCT TCC AGC TTC AAG AGG CGT				2739
Thr Phe Arg Ala Ile Thr Ser Thr Leu Ala Ser Ser Phe Lys Arg Arg				
815	820	825		
AGG TCC TCC AAA GAC ACG AGC ACC GGG GGT GGA CGC GGT GCT TTG CAA				2787
Arg Ser Ser Lys Asp Thr Ser Thr Gly Gly Arg Gly Ala Leu Gln				
830	835	840		
AAC CAA AAA GAC ACA GTG CTG CCG CGA CGC GCT ATT GAG AGG GAG GAG				2835
Asn Gln Lys Asp Thr Val Leu Pro Arg Arg Ala Ile Glu Arg Glu Glu				
845	850	855		
GGC CAG CTG CAG CTG TGT TCC CGT CAT AGG GAG AGC TGAGACTCCC				2881
Gly Gln Leu Gln Leu Cys Ser Arg His Arg Glu Ser				
860	865	870		
CGCCCCGCCCT CCTCTGCCCT CTCCCCCGCA GACAGACAGA CAGACGGACG GGACAGCGGC				2941
CCGGCCACG CAGAGCCCCG GAGCACACG GGGTCGGGGG AGGAGCACCC CCAGCCTCCC				3001
CCAGGCTGCG CCTGCCGCC CGCCGGTTGG CGGCTGGCC GGTCCACCCC GTCCCGGCC				3061
CGCGCGTGCC CCCAGCGTGG GGCTAACGGG CGCCTTGTCT GTGTATTCT ATTTTGCA				3121
AGTACCATCC CACTGATATC ACGGGCCCGC TCAACCTCTC AGATCCCTCG GTCAGCACCG				3181
TGGTGTGAGG CCCCCGGAGG CGCCCACCTG CCCAGTTAGC CCGGCCAAGG ACACTGATGG				3241
GTCCTGCTGC TCGGGAAAGGC CTGAGGGAAAG CCCACCCGCC CCAGAGACTG CCCACCCCTGG				3301
GCCTCCCGTC CGTCCGCCCG CCCACCCCGC TGCCTGGCG GCAGCCCTG CTGGACCAAG				3361
GTGCGGACCG GAGCGGCTGA GGACGGGGCA GAGCTGAGTC GGCTGGCAG GGCGCAGGG				3421
CGCTCCGGCA GAGGCAGGCC CCTGGGGTCT CTGAGCAGTG GGGAGCGGGG GCTAACTGCC				3481
CCCAGGGCGGA GGGGCTTGGG GCAGAGACGG CAGCCCCATC CTTCCCGCAG CACCAGCCTG				3541
AGCCACAGTG GGGCCCATGG CCCCAGCTGG CTGGTCGCC CCTCCTCGGG CGCCTGCGCT				3601
CCTCTGCAGC CTGAGCTCCA CCCTCCCCCTC TTCTTGCGGC ACCGCCACC AAACACCCCG				3661
TCTGCCCTT GACGCCACAC GCCGGGGCTG GCGCTGCCCT CCCCCACGGC CGTCCCTGAC				3721
TTCCCAAGCTG GCAGCGCCTC CGGCCGCCCTC GGGCCGCCCTC CTCCAGAAC GAGAGGGCTG				3781
AGCCCCCTCT CTCCTCGTCC GGCCTGCAGC ACAGAAGGGG GCCTCCCCGG GGGTCCCCGG				3841
ACGCTGGCTC GGGACTGTCT TCAACCCCTGC CCTGCACCTT GGGCACGGGA GAGCGCCACC				3901
CGCCCCGCCCT CGCCCTCGCT CGGGGTGCGT GACCGGCCCG CCACCTTGTA CAGAACCCAGC				3961
ACTCCCAGGG CCCGAGCGCG TGCCCTCCCC GTGCGCAGCC GCGCTCTGCC CCTCCGTCCC				4021
CAGGGTGCAG GCGCGCACCG CCCAACCCCCC ACCTCCGGT GTATGCAGTG GTGATGCCTA				4081

AAGGAATGTC ACG

4094

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 870 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Met Ser Thr Met Arg Leu Leu Thr Leu Ala Leu Leu Phe Ser Cys Ser
1 5 10 15

Val Ala Arg Ala Ala Cys Asp Pro Lys Ile Val Asn Ile Gly Ala Val
20 25 30

Leu Ser Thr Arg Lys His Glu Gln Met Phe Arg Glu Ala Val Asn Gln
35 40 45

Ala Asn Lys Arg His Gly Ser Trp Lys Ile Gln Leu Asn Ala Thr Ser
50 55 60

Val Thr His Lys Pro Asn Ala Ile Gln Met Ala Leu Ser Val Cys Glu
65 70 75 80

Asp Leu Ile Ser Ser Gln Val Tyr Ala Ile Leu Val Ser His Pro Pro
85 90 95

Thr Pro Asn Asp His Phe Thr Pro Thr Pro Val Ser Tyr Thr Ala Gly
100 105 110

Phe Tyr Arg Ile Pro Val Leu Gly Leu Thr Thr Arg Met Ser Ile Tyr
115 120 125

Ser Asp Lys Ser Ile His Leu Ser Phe Leu Arg Thr Val Pro Pro Tyr
130 135 140

Ser His Gln Ser Ser Val Trp Phe Glu Met Met Arg Val Tyr Ser Trp
145 150 155 160

Asn His Ile Ile Leu Leu Val Ser Asp Asp His Glu Gly Arg Ala Ala
165 170 175

Gln Lys Arg Leu Glu Thr Leu Leu Glu Arg Glu Ser Lys Ala Glu
180 185 190

Lys Val Leu Gln Phe Asp Pro Gly Thr Lys Asn Val Thr Ala Leu Leu
195 200 205

Met Glu Ala Lys Glu Leu Glu Ala Arg Val Ile Ile Leu Ser Ala Ser
210 215 220

Glu Asp Asp Ala Ala Thr Val Tyr Arg Ala Ala Met Leu Asn Met
225 230 235 240

Thr Gly Asn Thr Asn Ile Trp Lys Thr Gly Pro Leu Phe Lys Arg Val
245 250 255

Leu Met Ser Ser Lys Tyr Ala Asp Gly Val Thr Gly Arg Val Glu Phe
260 265 270

Asn Glu Asp Gly Asp Arg Lys Phe Ala Asn Tyr Ser Ile Met Asn Leu
275 280 285

Gln Asn Arg Lys Leu Val Gln Val Gly Ile Tyr Asn Gly Thr His Val
290 295 300

Ile Pro Asn Asp Arg Lys Ile Ile Trp Pro Gly Gly Glu Thr Glu Lys
305 310 315 320

Pro Arg Gly Tyr Gln Met Ser Thr Arg Leu Lys Ile Val Thr Ile His
325 330 335

Gln Glu Pro Phe Val Tyr Val Lys Pro Thr Leu Ser Asp Gly Thr Cys
340 345 350

Lys Glu Glu Phe Thr Val Asn Gly Asp Pro Val Lys Lys Val Ile Cys
355 360 365

Thr Gly Pro Asn Asp Thr Ser Pro Gly Ser Pro Arg His Thr Val Pro
370 375 380

Gln Cys Cys Tyr Gly Phe Cys Ile Asp Leu Leu Ile Lys Leu Ala Arg
385 390 395 400

Thr Met Asn Phe Thr Tyr Glu Val His Leu Val Ala Asp Gly Lys Phe
405 410 415

Gly Thr Gln Glu Arg Val Asn Asn Ser Asn Lys Lys Glu Trp Asn Gly
420 425 430

Met Met Gly Glu Leu Leu Ser Gly Gln Ala Asp Met Ile Val Ala Pro
435 440 445

Leu Thr Ile Asn Asn Glu Arg Ala Gln Tyr Ile Glu Phe Ser Lys Pro
450 455 460

Phe Lys Tyr Gln Gly Leu Thr Ile Leu Val Lys Lys Glu Ile Pro Arg
465 470 475 480

Ser Thr Leu Asp Ser Phe Met Gln Pro Phe Gln Ser Thr Leu Trp Leu
485 490 495

Leu Val Gly Leu Ser Val His Val Val Ala Val Met Leu Tyr Leu Leu
500 505 510

Asp Arg Phe Ser Pro Phe Gly Arg Phe Lys Val Asn Ser Glu Glu Glu
515 520 525

Glu Glu Asp Ala Leu Thr Leu Ser Ser Ala Met Trp Phe Ser Trp Gly
530 535 540

Val Leu Leu Asn Ser Gly Ile Gly Glu Gly Ala Pro Arg Ser Phe Ser
545 550 555 560

Ala Arg Ile Leu Gly Met Val Trp Ala Gly Phe Ala Met Ile Ile Val
565 570 575

Ala Ser Tyr Thr Ala Asn Leu Ala Ala Phe Leu Val Leu Asp Arg Pro
580 585 590

Glu Glu Arg Ile Thr Gly Ile Asn Asp Pro Arg Leu Arg Asn Pro Ser
595 600 605

Asp Lys Phe Ile Tyr Ala Thr Val Lys Gln Ser Ser Val Asp Ile Tyr
610 615 620

Phe Arg Arg Gln Val Glu Leu Ser Thr Met Tyr Arg His Met Glu Lys
625 630 635 640

His Asn Tyr Glu Ser Ala Ala Glu Ala Ile Gln Ala Val Arg Asp Asn

645

650

655

Lys Leu His Ala Phe Ile Trp Asp Ser Ala Val Leu Glu Phe Glu Ala
660 665 670

Ser Gln Lys Cys Asp Leu Val Thr Thr Gly Glu Leu Phe Phe Arg Ser
675 680 685

Gly Phe Gly Ile Gly Met Arg Lys Asp Ser Pro Trp Lys Gln Asn Val
690 695 700

Ser Leu Ser Ile Leu Lys Ser His Glu Asn Gly Phe Met Glu Asp Leu
705 710 715 720

Asp Lys Thr Trp Val Arg Tyr Gln Glu Cys Asp Ser Arg Ser Asn Ala
725 730 735

Pro Ala Thr Leu Thr Phe Glu Asn Met Ala Gly Val Phe Met Leu Val
740 745 750

Ala Gly Gly Ile Val Ala Gly Ile Phe Leu Ile Phe Ile Glu Ile Ala
755 760 765

Tyr Lys Arg His Lys Asp Ala Arg Arg Lys Gln Met Gln Leu Ala Phe
770 775 780

Ala Ala Val Asn Val Trp Arg Lys Asn Leu Gln Asp Arg Lys Ser Gly
785 790 795 800

Arg Ala Glu Pro Asp Pro Lys Lys Ala Thr Phe Arg Ala Ile Thr
805 810 815

Ser Thr Leu Ala Ser Ser Phe Lys Arg Arg Ser Ser Lys Asp Thr
820 825 830

Ser Thr Gly Gly Arg Gly Ala Leu Gln Asn Gln Lys Asp Thr Val
835 840 845

Leu Pro Arg Arg Ala Ile Glu Arg Glu Glu Gly Gln Leu Gln Leu Cys
850 855 860

Ser Arg His Arg Glu Ser
865 870

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3731 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 262..2826

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

CAAGCCGGGC GTTCGGAGCT GTGCCCGGCC CCGCTTCAGC ACCGCGGACA GCGCCGGCCG 60
CGTGGGGCTG AGCGCCGAGC CCCCGCGCAC GCTTCAGCCC CCCTTCCCTC GGCGGACGTC 120

CCGGGACCGC CGCTCCGGGG GAGACGTGGC GTCCGCAGCC CGTGGGGCG GGGGAGCGCA	180
GGACGGCCCG GAAGCCCCGC GGGGGATGCG CCGAGGGCCC CGCGTTCGCG CGCGCGAGAG	240
CCAGGGCCCGC GGCGTGAGCC C ATG AGC ACC ATG CGC CTG CTG ACG CTC GCC Met Ser Thr Met Arg Leu Leu Thr Leu Ala 1 5 10	291
CTG CTG TTC TCC TGC TCC GCC CGT GCC GCG TGC GAC CCC AAG ATC Leu Leu Phe Ser Cys Ser Val Ala Arg Ala Ala Cys Asp Pro Lys Ile 15 20 25	339
GTC AAC ATT GGC GCG GTG CTG AGC ACG CGG AAG CAC GAG CAG ATG TTC Val Asn Ile Gly Ala Val Leu Ser Thr Arg Lys His Glu Gln Met Phe 30 35 40	387
CGC GAG GCC GTG AAC CAG GCC AAC AAG CGG CAC GGC TCC TGG AAG ATT Arg Glu Ala Val Asn Gln Ala Asn Lys Arg His Gly Ser Trp Lys Ile 45 50 55	435
CAG CTC AAT GCC ACC TCC GTC ACG CAC AAG CCC AA GCC ATC CAG ATG Gln Leu Asn Ala Thr Ser Val Thr His Lys Pro Asn Ala Ile Gln Met 60 65 70	483
GCT CTG TCG GTG TGC GAG GAC CTC ATC TCC AGC CAG GTC TAC GCC ATC Ala Leu Ser Val Cys Glu Asp Leu Ile Ser Ser Gln Val Tyr Ala Ile 75 80 85 90	531
CTA GTT AGC CAT CCA CCT ACC CCC AAC GAC CAC TTC ACT CCC ACC CCT Leu Val Ser His Pro Pro Thr Pro Asn Asp His Phe Thr Pro Thr Pro 95 100 105	579
GTC TCC TAC ACA GCC GGC TTC TAC CGC ATA CCC GTG CTG GGG CTG ACC Val Ser Tyr Thr Ala Gly Phe Tyr Arg Ile Pro Val Leu Gly Leu Thr 110 115 120	627
ACC CGC ATG TCC ATC TAC TCG GAC AAG AGC ATC CAC CTG AGC TTC CTG Thr Arg Met Ser Ile Tyr Ser Asp Lys Ser Ile His Leu Ser Phe Leu 125 130 135	675
CGC ACC GTG CCG CCC TAC TCC CAC CAG TCC AGC GTG TGG TTT GAG ATG Arg Thr Val Pro Pro Tyr Ser His Gln Ser Ser Val Trp Phe Glu Met 140 145 150	723
ATG CGT GTC TAC AGC TGG AAC CAC ATC ATC CTG CTG GTC AGC GAC GAC Met Arg Val Tyr Ser Trp Asn His Ile Ile Leu Leu Val Ser Asp Asp 155 160 165 170	771
CAC GAG GGC CCG GCG GCT CAG AAA CGC CTG GAG ACG CTG CTG GAG GAG His Glu Gly Arg Ala Ala Gln Lys Arg Leu Glu Thr Leu Leu Glu Glu 175 180 185	819
CGT GAG TCC AAG GCA GAG AAG GTG CTG CAG TTT GAC CCA GGG ACC AAG Arg Glu Ser Lys Ala Glu Lys Val Leu Gln Phe Asp Pro Gly Thr Lys 190 195 200	867
AAC GTG ACG GCC CTG CTG ATG GAG GCG AAA GAG CTG GAG GCC CGG GTC Asn Val Thr Ala Leu Leu Met Glu Ala Lys Glu Leu Glu Ala Arg Val 205 210 215	915
ATC ATC CTT TCT GCC AGC GAG GAC GAT GCT GCC ACT GTA TAC CGC GCA Ile Ile Leu Ser Ala Ser Glu Asp Asp Ala Ala Thr Val Tyr Arg Ala 220 225 230	963
GCC GCG ATG CTG AAC ATG ACG GGC AAC ACC AAC ATC TGG AAG ACC GGG Ala Ala Met Leu Asn Met Thr Gly Asn Thr Asn Ile Trp Lys Thr Gly 235 240 245 250	1011

CCG CTC TTC AAG AGA GTG CTG ATG TCT TCC AAG TAT GCG GAT GGC GTG Pro Leu Phe Lys Arg Val Leu Met Ser Ser Lys Tyr Ala Asp Gly Val 255 260 265	1059
ACT GGT CGC GTG GAG TTC AAT GAG GAT GGG GAC GGG AAG TTC GGC AAC Thr Gly Arg Val Glu Phe Asn Glu Asp Gly Asp Arg Lys Phe Ala Asn 270 275 280	1107
TAC AGC ATC ATG AAC CTG CAG AAC CGC AAG CTG GTG CAA GTG GGC ATC Tyr Ser Ile Met Asn Leu Gln Asn Arg Lys Leu Val Gln Val Gly Ile 285 290 295	1155
TAC AAT GGC ACC CAC GTC ATC CCT AAT GAC AGG AAG ATC ATC TGG CCA Tyr Asn Gly Thr His Val Ile Pro Asn Asp Arg Lys Ile Ile Trp Pro 300 305 310	1203
GGC GGA GAG ACA GAG AAG CCT CGA GGG TAC CAG ATG TCC ACC AGA CTG Gly Gly Glu Thr Glu Lys Pro Arg Gly Tyr Gln Met Ser Thr Arg Leu 315 320 325 330	1251
AAG ATT GTG ACG ATC CAC CAG GAG CCC TTC GTG TAC GTC AAG CCC ACG Lys Ile Val Thr Ile His Gln Glu Pro Phe Val Tyr Val Lys Pro Thr 335 340 345	1299
CTG AGT GAT GGG ACA TGC AAG GAG GAG TTC ACA GTC AAC GGC GAC CCA Leu Ser Asp Gly Thr Cys Lys Glu Glu Phe Thr Val Asn Gly Asp Pro 350 355 360	1347
GTC AAG AAG GTG ATC TGC ACC GGG CCC AAC GAC ACG TCG CCG GGC AGC Val Lys Lys Val Ile Cys Thr Gly Pro Asn Asp Thr Ser Pro Gly Ser 365 370 375	1395
CCC CGC CAC ACG GTG CCT CAG TGT TGC TAC GGC TTT TGC ATC GAC CTG Pro Arg His Thr Val Pro Gln Cys Cys Tyr Gly Phe Cys Ile Asp Leu 380 385 390	1443
CTC ATC AAG CTG GCA CGG ACC ATG AAC TTC ACC TAC GAG GTG CAC CTG Leu Ile Lys Leu Ala Arg Thr Met Asn Phe Thr Tyr Glu Val His Leu 395 400 405 410	1491
GTG GCA GAT GGC AAG TTC GGC ACA CAG GAG CGG GTG AAC AAC AGC AAC Val Ala Asp Gly Lys Phe Gly Thr Gln Glu Arg Val Asn Asn Ser Asn 415 420 425	1539
AAG AAG GAG TGG AAT GGG ATG ATG GGC GAG CTG CTC AGC GGG CAG GCA Lys Lys Glu Trp Asn Gly Met Met Gly Glu Leu Leu Ser Gly Gln Ala 430 435 440	1587
GAC ATG ATC GTG GCG CCG CTA ACC ATA AAC AAC GAG CGC GCG CAG TAC Asp Met Ile Val Ala Pro Leu Thr Ile Asn Asn Glu Arg Ala Gln Tyr 445 450 455	1635
ATC GAG TTT TCC AAG CCC TTC AAG TAC CAG GGC CTG ACT ATT CTG GTC Ile Glu Phe Ser Lys Pro Phe Lys Tyr Gln Gly Leu Thr Ile Leu Val 460 465 470	1683
AAG AAG GAG ATT CCC CGG AGC ACG CTG GAC TCG TTC ATG CAG CGC TTC Lys Lys Glu Ile Pro Arg Ser Thr Leu Asp Ser Phe Met Gln Pro Phe 475 480 485 490	1731
CAG AGC ACA CTG TGG CTG CTG GTG GGG CTG TCG GTG CAC GTG GTG GGC Gln Ser Thr Leu Trp Leu Leu Val Gly Leu Ser Val His Val Val Ala 495 500 505	1779
GTG ATG CTG TAC CTG CTG GAC CGC TTC AGC CCC TTC GGC CGG TTC AAG Val Met Leu Tyr Leu Leu Asp Arg Phe Ser Pro Phe Gly Arg Phe Lys	1827

510	515	520	
GTG AAC AGC GAG GAG GAG GAC GCA CTG ACC CTG TCC TCG GCC Val Asn Ser Glu Glu Glu Glu Asp Ala Leu Thr Leu Ser Ser Ala 525	530	535	1875
ATG TGG TTC TCC TGG GGC GTC CTG CTC AAC TCC GGC ATC GGG GAA GGC Met Trp Phe Ser Trp Gly Val Leu Leu Asn Ser Gly Ile Gly Glu Gly 540	545	550	1923
GCC CCC AGA AGC TTC TCA GCG CGC ATC CTG GGC ATG GTG TGG GCC GGC Ala Pro Arg Ser Phe Ser Ala Arg Ile Leu Gly Met Val Trp Ala Gly 555	560	565	1971
TTT GCC ATG ATC ATC GTG GCC TCC TAC ACC GCC AAC CTG GCG GCC TTC Phe Ala Met Ile Ile Val Ala Ser Tyr Thr Ala Asn Leu Ala Ala Phe 575	580	585	2019
CTG GTG CTG GAC CGG CCG GAG GAG CGC ATC ACG GGC ATC AAC GAC CCT Leu Val Leu Asp Arg Pro Glu Glu Arg Ile Thr Gly Ile Asn Asp Pro 590	595	600	2067
CGG CTG AGG AAC CCC TCG GAC AAG TTT ATC TAC GCC ACG GTG AAG CAG Arg Leu Arg Asn Pro Ser Asp Lys Phe Ile Tyr Ala Thr Val Lys Gln 605	610	615	2115
AGC TCC GTG GAT ATC TAC TTC CGG CGC CAG GTG GAG CTG AGC ACC ATG Ser Ser Val Asp Ile Tyr Phe Arg Arg Gln Val Glu Leu Ser Thr Met 620	625	630	2163
TAC CGG CAT ATG GAG AAG CAC AAC TAC GAG AGT GCG GCG GAG GCC ATC Tyr Arg His Met Glu Lys His Asn Tyr Glu Ser Ala Ala Glu Ala Ile 635	640	645	2211
CAG GCC GTG AGA GAC AAC AAG CTG CAT GCC TTC ATC TGG GAC TCG GCG Gln Ala Val Arg Asp Asn Lys Leu His Ala Phe Ile Trp Asp Ser Ala 655	660	665	2259
GTG CTG GAG TTC GAG GCC TCG CAG AAG TGC GAC CTG GTG ACG ACT GGA Val Leu Glu Phe Glu Ala Ser Gln Lys Cys Asp Leu Val Thr Thr Gly 670	675	680	2307
GAG CTG TTT TTC CGC TCG GGC TTC GGC ATA GGC ATG CGC AAA GAC AGC Glu Leu Phe Phe Arg Ser Gly Phe Gly Ile Gly Met Arg Lys Asp Ser 685	690	695	2355
CCC TGG AAG CAG AAC GTC TCC CTG TCC ATC CTC AAG TCC CAC GAG AAT Pro Trp Lys Gln Asn Val Ser Leu Ser Ile Leu Lys Ser His Glu Asn 700	705	710	2403
GGC TTC ATG GAA GAC CTG GAC AAG ACG TGG GTT CGG TAT CAG GAA TGT Gly Phe Met Glu Asp Leu Asp Lys Thr Trp Val Arg Tyr Gln Glu Cys 715	720	725	2451
GAC TCG CGC AGC AAC GCC CCT GCG ACC CTT ACT TTT GAG AAC ATG GCC Asp Ser Arg Ser Asn Ala Pro Ala Thr Leu Thr Phe Glu Asn Met Ala 735	740	745	2499
GGG GTC TTC ATG CTG GTA GCT GGG GGC ATC GTG GCC GGG ATC TTC CTG Gly Val Phe Met Leu Val Ala Gly Gly Ile Val Ala Gly Ile Phe Leu 750	755	760	2547
ATT TTC ATC GAG ATT GCC TAC AAG CGG CAC AAG GAT GCT CGC CGG AAG Ile Phe Ile Glu Ile Ala Tyr Lys Arg His Lys Asp Ala Arg Arg Lys 765	770	775	2595
CAG ATG CAG CTG GCC TTT GCC GTT AAC GTG TGG CGG AAG AAC CTG			2643

Gln	Met	Gln	Leu	Ala	Phe	Ala	Ala	Val	Asn	Val	Trp	Arg	Lys	Asn	Leu		
780					785						790						
CAG	GAT	AGA	AAG	AGT	GGT	AGA	GCA	GAG	CCT	GAC	CCT	AAA	AAG	AAA	GCC	2691	
Gln	Asp	Arg	Lys	Ser	Gly	Arg	Ala	Glu	Pro	Asp	Pro	Lys	Lys	Lys	Ala		
795					800						805					810	
ACA	TTT	AGG	GCT	ATC	ACC	TCC	ACC	CTG	GCT	TCC	AGC	TTC	AAG	AGG	CGT	2739	
Thr	Phe	Arg	Ala	Ile	Thr	Ser	Thr	Leu	Ala	Ser	Ser	Phe	Lys	Arg	Arg		
	815							820				825					
AGG	TCC	TCC	AAA	GAC	ACG	CAG	TAC	CAT	CCC	ACT	GAT	ATC	ACG	GGC	CCG	2787	
Arg	Ser	Ser	Lys	Asp	Thr	Gln	Tyr	His	Pro	Thr	Asp	Ile	Thr	Gly	Pro		
	830						835					840					
CTC	AAC	CTC	TCA	GAT	CCC	TCG	GTC	AGC	ACC	GTG	GTG	TGAGGCC				2833	
Leu	Asn	Leu	Ser	Asp	Pro	Ser	Val	Ser	Thr	Val	Val						
	845						850				855						
GGAGGC	GGCCC	ACCTG	CCCCAG	TTAG	CCCCGG	CAAG	GAC	ACT	GAT	GGGT	CCT	GCT	GCT	CGGG		2893	
AAGGC	CTG	GAG	GGAAG	CCCAC	CCG	CCCC	CAGA	GA	CTG	CCCAC	CCT	GGG	CC	GTC	CGT		2953
GCC	CGCC	AC	CCC	GCTG	GG	GGG	CAGC	CC	CTG	CTG	GG	CA	AGG	TG	C		3013
GCT	GAGG	ACG	GGG	CAGAG	G	AGT	CGG	CTG	GG	CAGGG	CCG	AGG	CG	CG	AGAG		3073
AGG	CCC	CTG	GG	GGT	CT	CTG	GAG	CAG	GGGG	GCTAA	CTG	CCCC	CAG	G	GGAGGG		3133
TTG	GAG	CAGA	GAC	GGG	CAG	CC	ATC	CTT	CC	CGCAG	ACCA	GC	CTG	AG	CCA		3193
CAT	GGC	CCC	CA	GCT	GG	CTG	GGG	TG	CG	CCC	CTC	TG	CT	G	AGC		3253
CT	CC	AC	CC	CT	CT	CC	CT	CT	CC	CC	CT	CT	CC	CT	GC		3313
CA	CAC	GCC	GG	GCT	GG	CG	GCT	GC	CC	CT	CC	TG	AC	TC	GC		3373
GC	CT	CC	GC	GC	CT	CC	GC	CT	CC	CC	CT	CC	TC	CT	CC		3433
CG	TCC	GG	GC	AG	GC	AG	AG	AG	GG	GG	GC	CC	TC	GG	AC		3493
TG	TCT	CAAC	CCT	GCC	CTG	AC	CTT	GGG	CA	CGG	AG	AG	CG	CC	AC		3553
TC	GCT	CC	GG	TG	GT	GAC	CG	GG	CC	GG	AG	AG	CG	CC	AG		3613
GC	CGT	GC	CT	TCC	GT	GCG	CAG	CC	GG	CC	CT	CC	AG	GG	CG		3673
CA	CCG	CC	AA	CCCC	CAC	CTC	CC	GGT	GT	GT	TAT	G	CTAA	AG	GA		3731

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 854 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Met Ser Thr Met Arg Leu Leu Thr Leu Ala Leu Leu Phe Ser Cys Ser
1 5 10 15

Val Ala Arg Ala Ala Cys Asp Pro Lys Ile Val Asn Ile Gly Ala Val
20 25 30

Leu Ser Thr Arg Lys His Glu Gln Met Phe Arg Glu Ala Val Asn Gln
35 40 45

Ala Asn Lys Arg His Gly Ser Trp Lys Ile Gln Leu Asn Ala Thr Ser
50 55 60

Val Thr His Lys Pro Asn Ala Ile Gln Met Ala Leu Ser Val Cys Glu
65 70 75 80

Asp Leu Ile Ser Ser Gln Val Tyr Ala Ile Leu Val Ser His Pro Pro
85 90 95

Thr Pro Asn Asp His Phe Thr Pro Thr Pro Val Ser Tyr Thr Ala Gly
100 105 110

Phe Tyr Arg Ile Pro Val Leu Gly Leu Thr Thr Arg Met Ser Ile Tyr
115 120 125

Ser Asp Lys Ser Ile His Leu Ser Phe Leu Arg Thr Val Pro Pro Tyr
130 135 140

Ser His Gln Ser Ser Val Trp Phe Glu Met Met Arg Val Tyr Ser Trp
145 150 155 160

Asn His Ile Ile Leu Leu Val Ser Asp Asp His Glu Gly Arg Ala Ala
165 170 175

Gln Lys Arg Leu Glu Thr Leu Leu Glu Glu Arg Glu Ser Lys Ala Glu
180 185 190

Lys Val Leu Gln Phe Asp Pro Gly Thr Lys Asn Val Thr Ala Leu Leu
195 200 205

Met Glu Ala Lys Glu Leu Glu Ala Arg Val Ile Ile Leu Ser Ala Ser
210 215 220

Glu Asp Asp Ala Ala Thr Val Tyr Arg Ala Ala Met Leu Asn Met
225 230 235 240

Thr Gly Asn Thr Asn Ile Trp Lys Thr Gly Pro Leu Phe Lys Arg Val
245 250 255

Leu Met Ser Ser Lys Tyr Ala Asp Gly Val Thr Gly Arg Val Glu Phe
260 265 270

Asn Glu Asp Gly Asp Arg Lys Phe Ala Asn Tyr Ser Ile Met Asn Leu
275 280 285

Gln Asn Arg Lys Leu Val Gln Val Gly Ile Tyr Asn Gly Thr His Val
290 295 300

Ile Pro Asn Asp Arg Lys Ile Ile Trp Pro Gly Gly Glu Thr Glu Lys
305 310 315 320

Pro Arg Gly Tyr Gln Met Ser Thr Arg Leu Lys Ile Val Thr Ile His
325 330 335

Gln Glu Pro Phe Val Tyr Val Lys Pro Thr Leu Ser Asp Gly Thr Cys
340 345 350

Lys Glu Glu Phe Thr Val Asn Gly Asp Pro Val Lys Lys Val Ile Cys
355 360 365

Thr Gly Pro Asn Asp Thr Ser Pro Gly Ser Pro Arg His Thr Val Pro
370 375 380

Gln Cys Cys Tyr Gly Phe Cys Ile Asp Leu Leu Ile Lys Leu Ala Arg

385

390

395

400

Thr Met Asn Phe Thr Tyr Glu Val His Leu Val Ala Asp Gly Lys Phe
405 410 415

Gly Thr Gln Glu Arg Val Asn Asn Ser Asn Lys Lys Glu Trp Asn Gly
420 425 430

Met Met Gly Glu Leu Leu Ser Gly Gln Ala Asp Met Ile Val Ala Pro
435 440 445

Leu Thr Ile Asn Asn Glu Arg Ala Gln Tyr Ile Glu Phe Ser Lys Pro
450 455 460

Phe Lys Tyr Gln Gly Leu Thr Ile Leu Val Lys Lys Glu Ile Pro Arg
465 470 475 480

Ser Thr Leu Asp Ser Phe Met Gln Pro Phe Gln Ser Thr Leu Trp Leu
485 490 495

Leu Val Gly Leu Ser Val His Val Val Ala Val Met Leu Tyr Leu Leu
500 505 510

Asp Arg Phe Ser Pro Phe Gly Arg Phe Lys Val Asn Ser Glu Glu Glu
515 520 525

Glu Glu Asp Ala Leu Thr Leu Ser Ser Ala Met Trp Phe Ser Trp Gly
530 535 540

Val Leu Leu Asn Ser Gly Ile Gly Glu Gly Ala Pro Arg Ser Phe Ser
545 550 555 560

Ala Arg Ile Leu Gly Met Val Trp Ala Gly Phe Ala Met Ile Ile Val
565 570 575

Ala Ser Tyr Thr Ala Asn Leu Ala Ala Phe Leu Val Leu Asp Arg Pro
580 585 590

Glu Glu Arg Ile Thr Gly Ile Asn Asp Pro Arg Leu Arg Asn Pro Ser
595 600 605

Asp Lys Phe Ile Tyr Ala Thr Val Lys Gln Ser Ser Val Asp Ile Tyr
610 615 620

Phe Arg Arg Gln Val Glu Leu Ser Thr Met Tyr Arg His Met Glu Lys
625 630 635 640

His Asn Tyr Glu Ser Ala Ala Glu Ala Ile Gln Ala Val Arg Asp Asn
645 650 655

Lys Leu His Ala Phe Ile Trp Asp Ser Ala Val Leu Glu Phe Glu Ala
660 665 670

Ser Gln Lys Cys Asp Leu Val Thr Thr Gly Glu Leu Phe Phe Arg Ser
675 680 685

Gly Phe Gly Ile Gly Met Arg Lys Asp Ser Pro Trp Lys Gln Asn Val
690 695 700

Ser Leu Ser Ile Leu Lys Ser His Glu Asn Gly Phe Met Glu Asp Leu
705 710 715 720

Asp Lys Thr Trp Val Arg Tyr Gln Glu Cys Asp Ser Arg Ser Asn Ala
725 730 735

Pro Ala Thr Leu Thr Phe Glu Asn Met Ala Gly Val Phe Met Leu Val

740

745

750

Ala Gly Gly Ile Val Ala Gly Ile Phe Leu Ile Phe Ile Glu Ile Ala
755 760 765

Tyr Lys Arg His Lys Asp Ala Arg Arg Lys Gln Met Gln Leu Ala Phe
770 775 780

Ala Ala Val Asn Val Trp Arg Lys Asn Leu Gln Asp Arg Lys Ser Gly
785 790 795 800

Arg Ala Glu Pro Asp Pro Lys Lys Ala Thr Phe Arg Ala Ile Thr
805 810 815

Ser Thr Leu Ala Ser Ser Phe Lys Arg Arg Ser Ser Lys Asp Thr
820 825 830

Gln Tyr His Pro Thr Asp Ile Thr Gly Pro Leu Asn Leu Ser Asp Pro
835 840 845

Ser Val Ser Thr Val Val
850

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3007 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 262..2988

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

CAAGCCGGGC GTTCGGAGCT GTGCCCGGCC CCGCTTCAGC ACCGCGGACA GCGCCGGCCG	60
CGTGGGGCTG AGCGCCGAGC CCCCGCGCAC GCTTCAGCCC CCCTTCCCTC GGCGGACGTC	120
CCGGGACCGC CGCTCCGGGG GAGACGTGGC GTCCGCAGCC CGCGGGGCCG GGCGAGCGCA	180
GGACGGCCCG GAAGCCCCGC GGGGGATGCG CCGAGGGCCC CGCGTTCGCG CCGCGCAGAG	240
CCAGGCCCCGC GGCCCGAGCC C ATG AGC ACC ATG CGC CTG CTG ACG CTC GCC	291
Met Ser Thr Met Arg Leu Leu Thr Leu Ala	
1 5 10	
CTG CTG TTC TCC TGC TCC GTC GCC CGT GCC GCG TGC GAC CCC AAG ATC	339
Leu Leu Phe Ser Cys Ser Val Ala Arg Ala Ala Cys Asp Pro Lys Ile	
15 20 25	
GTC AAC ATT GGC GCG GTG CTG AGC ACG CGG AAG CAC GAG CAG ATG TTC	387
Val Asn Ile Gly Ala Val Leu Ser Thr Arg Lys His Glu Gln Met Phe	
30 35 40	
CGC GAG GCC GTG AAC CAG GCC AAC AAG CGG CAC GGC TCC TGG AAG ATT	435
Arg Glu Ala Val Asn Gln Ala Asn Lys Arg His Gly Ser Trp Lys Ile	
45 50 55	

CAG CTC AAT GCC ACC TCC GTC ACG CAC AAG CCC AAC GCC ATC CAG ATG Gln Leu Asn Ala Thr Ser Val Thr His Lys Pro Asn Ala Ile Gln Met	483
60 65 70	
GCT CTG TCG GTG TGC GAG GAC CTC ATC TCC AGC CAG GTC TAC GCC ATC Ala Leu Ser Val Cys Glu Asp Leu Ile Ser Ser Gln Val Tyr Ala Ile	531
75 80 85 90	
CTA GTT AGC CAT CCA CCT ACC CCC AAC GAC CAC TTC ACT CCC ACC CCT Leu Val Ser His Pro Pro Thr Pro Asn Asp His Phe Thr Pro Thr Pro	579
95 100 105	
GTC TCC TAC ACA GCC GGC TTC TAC CGC ATA CCC GTG CTG GGG CTG ACC Val Ser Tyr Thr Ala Gly Phe Tyr Arg Ile Pro Val Leu Gly Leu Thr	627
110 115 120	
ACC CGC ATG TCC ATC TAC TCG GAC AAG AGC ATC CAC CTG AGC TTC CTG Thr Arg Met Ser Ile Tyr Ser Asp Lys Ser Ile His Leu Ser Phe Leu	675
125 130 135	
CGC ACC GTG CCG CCC TAC TCC CAC CAG TCC AGC GTG TGG TTT GAG ATG Arg Thr Val Pro Pro Tyr Ser His Gln Ser Ser Val Trp Phe Glu Met	723
140 145 150	
ATG CGT GTC TAC AGC TGG AAC CAC ATC ATC CTG CTG GTC AGC GAC GAC Met Arg Val Tyr Ser Trp Asn His Ile Ile Leu Leu Val Ser Asp Asp	771
155 160 165 170	
CAC GAG GGC CGG GCG GCT CAG AAA CGC CTG GAG ACG CTG CTG GAG GAG His Glu Gly Arg Ala Ala Gln Lys Arg Leu Glu Thr Leu Leu Glu Glu	819
175 180 185	
CGT GAG TCC AAG GCA GAG AAG GTG CTG CAG TTT GAC CCA GGG ACC AAG Arg Glu Ser Lys Ala Glu Lys Val Leu Gln Phe Asp Pro Gly Thr Lys	867
190 195 200	
AAC GTG ACG GCC CTG CTG ATG GAG GCG AAA GAG CTG GAG GCC CGG GTC Asn Val Thr Ala Leu Leu Met Glu Ala Lys Glu Leu Glu Ala Arg Val	915
205 210 215	
ATC ATC CTT TCT GCC AGC GAG GAC GAT GCT GCC ACT GTA TAC CGC GCA Ile Ile Leu Ser Ala Ser Glu Asp Asp Ala Ala Thr Val Tyr Arg Ala	963
220 225 230	
GCC GCG ATG CTG AAC ATG ACG GGC AAC ACC AAC ATC TGG AAG ACC GGG Ala Ala Met Leu Asn Met Thr Gly Asn Thr Asn Ile Trp Lys Thr Gly	1011
235 240 245 250	
CCG CTC TTC AAG AGA GTG CTG ATG TCT TCC AAG TAT GCG GAT GGG GTG Pro Leu Phe Lys Arg Val Leu Met Ser Ser Lys Tyr Ala Asp Gly Val	1059
255 260 265	
ACT GGT CGC GTG GAG TTC AAT GAG GAT GGG GAC CGG AAG TTC GCC AAC Thr Gly Arg Val Glu Phe Asn Glu Asp Gly Asp Arg Lys Phe Ala Asn	1107
270 275 280	
TAC AGC ATC ATG AAC CTG CAG AAC CGC AAG CTG GTG CAA GTG GGC ATC Tyr Ser Ile Met Asn Leu Gln Asn Arg Lys Leu Val Gln Val Gly Ile	1155
285 290 295	
TAC AAT GGC ACC CAC GTC ATC CCT AAT GAC AGG AAG ATC ATC TGG CCA Tyr Asn Gly Thr His Val Ile Pro Asn Asp Arg Lys Ile Ile Trp Pro	1203
300 305 310	
GGC GGA GAG ACA GAG AAG CCT CGA GGG TAC CAG ATG TCC ACC AGA CTG Gly Gly Glu Thr Glu Lys Pro Arg Gly Tyr Gln Met Ser Thr Arg Leu	1251
315 320 325 330	

AAG ATT GTG ACG ATC CAC CAG GAG CCC TTC GTG TAC GTC AAG CCC ACG	1299
Lys Ile Val Thr Ile His Gin Glu Pro Phe Val Tyr Val Lys Pro Thr	
335 340 345	
CTG AGT GAT GGG ACA TGC AAG GAG GAG TTC ACA GTC AAC GGC GAC CCA	1347
Leu Ser Asp Gly Thr Cys Lys Glu Phe Thr Val Asn Gly Asp Pro	
350 355 360	
GTC AAG AAG GTG ATC TGC ACC GGG CCC AAC GAC ACG TCG CCG GGC AGC	1395
Val Lys Val Ile Cys Thr Gly Pro Asn Asp Thr Ser Pro Gly Ser	
365 370 375	
CCC CGC CAC ACG GTG CCT CAG TGT TGC TAC GGC TTT TGC ATC GAC CTG	1443
Pro Arg His Thr Val Pro Gln Cys Cys Tyr Gly Phe Cys Ile Asp Leu	
380 385 390	
CTC ATC AAG CTG GCA CGG ACC ATG AAC TTC ACC TAC GAG GTG CAC CTG	1491
Leu Ile Lys Leu Ala Arg Thr Met Asn Phe Thr Tyr Glu Val His Leu	
395 400 405 410	
GTG GCA GAT GGC AAG TTC GGC ACA CAG GAG CGG GTG AAC AAC AGC AAC	1539
Val Ala Asp Gly Lys Phe Gly Thr Gln Glu Arg Val Asn Asn Ser Asn	
415 420 425	
AAG AAG GAG TGG AAT GGG ATG ATG GGC GAG CTG CTC AGC GGG CAG GCA	1587
Lys Lys Glu Trp Asn Gly Met Met Gly Glu Leu Leu Ser Gly Gln Ala	
430 435 440	
GAC ATG ATC GTG GCG CCG CTA ACC ATA AAC AAC GAG CGC GCG CAG TAC	1635
Asp Met Ile Val Ala Pro Leu Thr Ile Asn Asn Glu Arg Ala Gln Tyr	
445 450 455	
ATC GAG TTT TCC AAG CCC TTC AAG TAC CAG GGC CTG ACT ATT CTG GTC	1683
Ile Glu Phe Ser Lys Pro Phe Lys Tyr Gln Gly Leu Thr Ile Leu Val	
460 465 470	
AAG AAG GAG ATT CCC CGG AGC ACG CTG GAC TCG TTC ATG CAG CCG TTC	1731
Lys Lys Glu Ile Pro Arg Ser Thr Leu Asp Ser Phe Met Gln Pro Phe	
475 480 485 490	
CAG AGC ACA CTG TGG CTG CTG GTG GGG CTG TCG GTG CAC GTG GTG GCC	1779
Gln Ser Thr Leu Trp Leu Leu Val Gly Leu Ser Val His Val Val Ala	
495 500 505	
GTG ATG CTG TAC CTG GAC CGC TTC AGC CCC TTC GGC CGG TTC AAG	1827
Val Met Leu Tyr Leu Leu Asp Arg Phe Ser Pro Phe Gly Arg Phe Lys	
510 515 520	
GTG AAC AGC GAG GAG GAG GAC GCA CTG ACC CTG TCC TCG GCC	1875
Val Asn Ser Glu Glu Glu Asp Ala Leu Thr Leu Ser Ser Ala	
525 530 535	
ATG TGG TTC TCC TGG GGC GTC CTG CTC AAC TCC GGC ATC GGG GAA GGC	1923
Met Trp Phe Ser Trp Gly Val Leu Leu Asn Ser Gly Ile Gly Glu Gly	
540 545 550	
GCC CCC AGA AGC TTC TCA GCG CGC ATC CTG GGC ATG GTG TGG GCC GGC	1971
Ala Pro Arg Ser Phe Ser Ala Arg Ile Leu Gly Met Val Trp Ala Gly	
555 560 565 570	
TTT GCC ATG ATC ATC GTG GCC TCC TAC ACC GCC AAC CTG GCG GCC TTC	2019
Phe Ala Met Ile Ile Val Ala Ser Tyr Thr Ala Asn Leu Ala Ala Phe	
575 580 585	
CTG GTG CTG GAC CGG CCG GAG GAG CGC ATC ACG GGC ATC AAC GAC CCT	2067
Leu Val Leu Asp Arg Pro Glu Glu Arg Ile Thr Gly Ile Asn Asp Pro	
590 595 600	

CGG CTG AGG AAC CCC TCG GAC AAG TTT ATC TAC GCC ACG GTG AAG CAG Arg Leu Arg Asn Pro Ser Asp Lys Phe Ile Tyr Ala Thr Val Lys Gln 605 610 615	211
AGC TCC GTG GAT ATC TAC TTC CGG CGC CAG GTG GAG CTG AGC ACC ATG Ser Ser Val Asp Ile Tyr Phe Arg Arg Gln Val Glu Leu Ser Thr Met 620 625 630	2161
TAC CGG CAT ATG GAG AAG CAC AAC TAC GAG AGT GCG GCG GAG GCC ATC Tyr Arg His Met Glu Lys His Asn Tyr Glu Ser Ala Ala Glu Ala Ile 635 640 645 650	2211
CAG GCC GTG AGA GAC AAC AAG CTG CAT GCC TTC ATC TGG GAC TCG GCG Gln Ala Val Arg Asp Asn Lys Leu His Ala Phe Ile Trp Asp Ser Ala 655 660 665	2259
GTG CTG GAG TTC GAG GCC TCG CAG AAG TGC GAC CTG GTG ACG ACT GGA Val Leu Glu Phe Glu Ala Ser Gln Lys Cys Asp Leu Val Thr Thr Gly 670 675 680	2307
GAG CTG TTT TTC CGC TCG GGC TTC GGC ATA GGCG ATG CGC AAA GAC AGC Glu Leu Phe Phe Arg Ser Gly Phe Gly Ile Gly Met Arg Lys Asp Ser 685 690 695	2355
CCC TGG AAG CAG AAC GTC TCC CTG TCC ATC CTC AAG TCC CAC GAG AAT Pro Trp Lys Gln Asn Val Ser Leu Ser Ile Leu Lys Ser His Glu Asn 700 705 710	2403
GGC TTC ATG GAA GAC CTG GAC AAG ACG TGG GTT CGG TAT CAG GAA TGT Gly Phe Met Glu Asp Leu Asp Lys Thr Trp Val Arg Tyr Gln Glu Cys 715 720 725 730	2451
GAC TCG CGC AGC AAC GCC CCT GCG ACC CTT ACT TTT GAG AAC ATG GCC Asp Ser Arg Ser Asn Ala Pro Ala Thr Leu Thr Phe Glu Asn Met Ala 735 740 745	2489
GGG GTC TTC ATG CTG GTA GCT GGG GGC ATC GTG GCC GGG ATC TTC CTG Gly Val Phe Met Leu Val Ala Gly Ile Val Ala Gly Ile Phe Leu 750 755 760	2547
ATT TTC ATC GAG ATT GCC TAC AAG CGG CAC AAG GAT GCT CGC CGG AAG Ile Phe Ile Glu Ile Ala Tyr Lys Arg His Lys Asp Ala Arg Arg Lys 765 770 775	2595
CAG ATG CAG CTG GCC TTT GCC GCC GTT AAC GTG TGG CGG AAG AAC CTG Gln Met Gln Leu Ala Phe Ala Ala Val Asn Val Trp Arg Lys Asn Leu 780 785 790	2643
CAG GAT AGA AAG AGT GGT AGA GCA GAG CCT GAC CCT AAA AAG AAA GCC Gln Asp Arg Lys Ser Gly Arg Ala Glu Pro Asp Pro Lys Lys Lys Ala 795 800 805 810	2691
ACA TTT AGG GCT ATC ACC TCC ACC CTG GCT TCC AGC TTC AAG AGG CGT Thr Phe Arg Ala Ile Thr Ser Thr Leu Ala Ser Ser Phe Lys Arg Arg 815 820 825	2739
AGG TCC TCC AAA GAC ACG CTG GCT CGG GAC TGT CTT CAA CCC TGC CCT Arg Ser Ser Lys Asp Thr Leu Ala Arg Asp Cys Leu Gln Pro Cys Pro 830 835 840	2787
GCA CCT TGG GCA CGG GAG AGC GCC ACC CGC CCG CCC CCG CCC TCG CTC Ala Pro Trp Ala Arg Glu Ser Ala Thr Arg Pro Pro Pro Pro Ser Leu 845 850 855	2835
CGG GTG CGT GAC CGG CCC GCC ACC TTG TAC AGA ACC AGC ACT CCC AGG Arg Val Arg Asp Arg Pro Ala Thr Leu Tyr Arg Thr Ser Thr Pro Arg 860 865 870	2883

GCC CGA GCG CGT GCC TTC CCC GTG CGC AGC CGC GCT CTG CCC CTC CGT Ala Arg Ala Arg Ala Phe Pro Val Arg Ser Arg Ala Leu Pro Leu Arg 875 880 885 890	2931
CCC CAG GGT GCA GGC GCG CAC CGC CCA ACC CCC ACC TCC CGG TGT ATG Pro Gln Gly Ala Gly Ala His Arg Pro Thr Pro Thr Ser Arg Cys Met 895 900 905	2979
CAG TGG TGATGCCTAA AGGAATGTCA CG Gln Trp	3007

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 908 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Met Ser Thr Met Arg Leu Leu Thr Leu Ala Leu Leu Phe Ser Cys Ser 1 5 10 15
Val Ala Arg Ala Ala Cys Asp Pro Lys Ile Val Asn Ile Gly Ala Val 20 25 30
Leu Ser Thr Arg Lys His Glu Gln Met Phe Arg Glu Ala Val Asn Gln 35 40 45
Ala Asn Lys Arg His Gly Ser Trp Lys Ile Gln Leu Asn Ala Thr Ser 50 55 60
Val Thr His Lys Pro Asn Ala Ile Gln Met Ala Leu Ser Val Cys Glu 65 70 75 80
Asp Leu Ile Ser Ser Gln Val Tyr Ala Ile Leu Val Ser His Pro Pro 85 90 95
Thr Pro Asn Asp His Phe Thr Pro Thr Pro Val Ser Tyr Thr Ala Gly 100 105 110
Phe Tyr Arg Ile Pro Val Leu Gly Leu Thr Thr Arg Met Ser Ile Tyr 115 120 125
Ser Asp Lys Ser Ile His Leu Ser Phe Leu Arg Thr Val Pro Pro Tyr 130 135 140
Ser His Gln Ser Ser Val Trp Phe Glu Met Met Arg Val Tyr Ser Trp 145 150 155 160
Asn His Ile Ile Leu Leu Val Ser Asp Asp His Glu Gly Arg Ala Ala 165 170 175
Gln Lys Arg Leu Glu Thr Leu Leu Glu Glu Arg Glu Ser Lys Ala Glu 180 185 190
Lys Val Leu Gln Phe Asp Pro Gly Thr Lys Asn Val Thr Ala Leu Leu 195 200 205
Met Glu Ala Lys Glu Leu Glu Ala Arg Val Ile Ile Leu Ser Ala Ser 210 215 220
Glu Asp Asp Ala Ala Thr Val Tyr Arg Ala Ala Met Leu Asn Met

225	230	235	240
Thr Gly Asn Thr Asn Ile Trp Lys Thr Gly Pro Leu Phe Lys Arg Val			
245	250	255	
Leu Met Ser Ser Lys Tyr Ala Asp Gly Val Thr Gly Arg Val Glu Phe			
260	265	270	
Asn Glu Asp Gly Asp Arg Lys Phe Ala Asn Tyr Ser Ile Met Asn Leu			
275	280	285	
Gln Asn Arg Lys Leu Val Gln Val Gly Ile Tyr Asn Gly Thr His Val			
290	295	300	
Ile Pro Asn Asp Arg Lys Ile Ile Trp Pro Gly Gly Glu Thr Glu Lys			
305	310	315	320
Pro Arg Gly Tyr Gln Met Ser Thr Arg Leu Lys Ile Val Thr Ile His			
325	330	335	
Gln Glu Pro Phe Val Tyr Val Lys Pro Thr Leu Ser Asp Gly Thr Cys			
340	345	350	
Lys Glu Glu Phe Thr Val Asn Gly Asp Pro Val Lys Lys Val Ile Cys			
355	360	365	
Thr Gly Pro Asn Asp Thr Ser Pro Gly Ser Pro Arg His Thr Val Pro			
370	375	380	
Gln Cys Cys Tyr Gly Phe Cys Ile Asp Leu Leu Ile Lys Leu Ala Arg			
385	390	395	400
Thr Met Asn Phe Thr Tyr Glu Val His Leu Val Ala Asp Gly Lys Phe			
405	410	415	
Gly Thr Gln Glu Arg Val Asn Asn Ser Asn Lys Lys Glu Trp Asn Gly			
420	425	430	
Met Met Gly Glu Leu Leu Ser Gly Gln Ala Asp Met Ile Val Ala Pro			
435	440	445	
Leu Thr Ile Asn Asn Glu Arg Ala Gln Tyr Ile Glu Phe Ser Lys Pro			
450	455	460	
Phe Lys Tyr Gln Gly Leu Thr Ile Leu Val Lys Lys Glu Ile Pro Arg			
465	470	475	480
Ser Thr Leu Asp Ser Phe Met Gln Pro Phe Gln Ser Thr Leu Trp Leu			
485	490	495	
Leu Val Gly Leu Ser Val His Val Val Ala Val Met Leu Tyr Leu Leu			
500	505	510	
Asp Arg Phe Ser Pro Phe Gly Arg Phe Lys Val Asn Ser Glu Glu Glu			
515	520	525	
Glu Glu Asp Ala Leu Thr Leu Ser Ser Ala Met Trp Phe Ser Trp Gly			
530	535	540	
Val Leu Leu Asn Ser Gly Ile Gly Glu Gly Ala Pro Arg Ser Phe Ser			
545	550	555	560
Ala Arg Ile Leu Gly Met Val Trp Ala Gly Phe Ala Met Ile Ile Val			
565	570	575	
Ala Ser Tyr Thr Ala Asn Leu Ala Ala Phe Leu Val Leu Asp Arg Pro			
580	585	590	

Glu Glu Arg Ile Thr Gly Ile Asn Asp Pro Arg Leu Arg Asn Pro Ser
557 600 605

Asp Lys Phe Ile Tyr Ala Thr Val Lys Gln Ser Ser Val Asp Ile Tyr
610 615 620

Phe Arg Arg Gln Val Glu Leu Ser Thr Met Tyr Arg His Met Glu Lys
625 630 635 640

His Asn Tyr Glu Ser Ala Ala Glu Ala Ile Gln Ala Val Arg Asp Asn
645 650 655

Lys Leu His Ala Phe Ile Trp Asp Ser Ala Val Leu Glu Phe Glu Ala
660 665 670

Ser Gln Lys Cys Asp Leu Val Thr Thr Gly Glu Leu Phe Phe Arg Ser
675 680 685

Gly Phe Gly Ile Gly Met Arg Lys Asp Ser Pro Trp Lys Gln Asn Val
690 695 700

Ser Leu Ser Ile Leu Lys Ser His Glu Asn Gly Phe Met Glu Asp Leu
705 710 715 720

Asp Lys Thr Trp Val Arg Tyr Gln Glu Cys Asp Ser Arg Ser Asn Ala
725 730 735

Pro Ala Thr Leu Thr Phe Glu Asn Met Ala Gly Val Phe Met Leu Val
740 745 750

Ala Gly Gly Ile Val Ala Gly Ile Phe Leu Ile Phe Ile Glu Ile Ala
755 760 765

Tyr Lys Arg His Lys Asp Ala Arg Arg Lys Gln Met Gln Leu Ala Phe
770 775 780

Ala Ala Val Asn Val Trp Arg Lys Asn Leu Gln Asp Arg Lys Ser Gly
785 790 795 800

Arg Ala Glu Pro Asp Pro Lys Lys Ala Thr Phe Arg Ala Ile Thr
805 810 815

Ser Thr Leu Ala Ser Ser Phe Lys Arg Arg Arg Ser Ser Lys Asp Thr
820 825 830

Leu Ala Arg Asp Cys Leu Gln Pro Cys Pro Ala Pro Trp Ala Arg Glu
835 840 845

Ser Ala Thr Arg Pro Pro Pro Ser Leu Arg Val Arg Asp Arg Pro
850 855 860

Ala Thr Leu Tyr Arg Thr Ser Thr Pro Arg Ala Arg Ala Arg Ala Phe
865 870 875 880

Pro Val Arg Ser Arg Ala Leu Pro Leu Arg Pro Gln Gly Ala Gly Ala
885 890 895

His Arg Pro Thr Pro Thr Ser Arg Cys Met Gln Trp
900 905

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3998 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: both
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 262..3093

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

CAAGCCGGGC GTTCGGAGCT GTGCCCGGCC CCGCTTCAGC ACCGGGACA GCGCCGGCCG	60
CGTGGGGCTG AGCGCCGAGC CCCCGCGCAC GCTTCAGCCC CCCTTCCCTC GGCGACGTC	120
CCGGGACCGC CGCTCCGGGG GAGACGTGGC GTCCGCAGCC CGCGGGGCCG GGCGAGCGCA	180
GGACGGCCCG GAAGCCCCGC GGGGGATGCG CCGAGGGCCC CGCGTTCGCG CGCGCAGAG	240
CCAGGCCCGC GGCCCGAGCC C ATG AGC ACC ATG CGC CTG CTG ACG CTC GCC	291
Met Ser Thr Met Arg Leu Leu Thr Leu Ala	
1 5 10	
CTG CTG TTC TCC TGC TCC GTC GCC CGT GCC GCG TGC GAC CCC AAG ATC	339
Leu Leu Phe Ser Cys Ser Val Ala Arg Ala Cys Asp Pro Lys Ile	
15 20 25	
GTC AAC ATT GGC GCG GTG CTG AGC ACG CGG AAG CAC GAG CAG ATG TTC	387
Val Asn Ile Gly Ala Val Leu Ser Thr Arg Lys His Glu Gln Met Phe	
30 35 40	
CGC GAG GCC GTG AAC CAG GCC AAC AAG CGG CAC GGC TCC TGG AAG ATT	435
Arg Glu Ala Val Asn Gln Ala Asn Lys Arg His Gly Ser Trp Lys Ile	
45 50 55	
CAG CTC AAT GCC ACC TCC GTC ACG CAC AAG CCC AAC GCC ATC CAG ATG	483
Gln Leu Asn Ala Thr Ser Val Thr His Lys Pro Asn Ala Ile Gln Met	
60 65 70	
GCT CTG TCG GTG TGC GAG GAC CTC ATC TCC AGC CAG GTC TAC GCC ATC	531
Ala Leu Ser Val Cys Glu Asp Leu Ile Ser Ser Gln Val Tyr Ala Ile	
75 80 85 90	
CTA GTT AGC CAT CCA CCT ACC CCC AAC GAC CAC TTC ACT CCC ACC CCT	579
Leu Val Ser His Pro Pro Thr Pro Asn Asp His Phe Thr Pro Thr Pro	
95 100 105	
GTC TCC TAC ACA GCC GGC TTC TAC CGC ATA CCC GTG CTG GGG CTG ACC	627
Val Ser Tyr Thr Ala Gly Phe Tyr Arg Ile Pro Val Leu Gly Leu Thr	
110 115 120	
ACC CGC ATG TCC ATC TAC TCG GAC AAG AGC ATC CAC CTG AGC TTC CTG	675
Thr Arg Met Ser Ile Tyr Ser Asp Lys Ser Ile His Leu Ser Phe Leu	
125 130 135	
CGC ACC GTG CCG CCC TAC TCC CAC CAG TCC AGC GTG TGG TTT GAG ATG	723
Arg Thr Val Pro Pro Tyr Ser His Gln Ser Ser Val Trp Phe Glu Met	
140 145 150	
ATG CGT GTC TAC AGC TGG AAC CAC ATC ATC CTG CTG GTC AGC GAC GAC	771
Met Arg Val Tyr Ser Trp Asn His Ile Ile Leu Leu Val Ser Asp Asp	
155 160 165 170	
CAC GAG GGC CGG GCG GCT CAG AAA CGC CTG GAG ACG CTG CTG GAG GAG	819
His Glu Gly Arg Ala Ala Gln Lys Arg Leu Glu Thr Leu Leu Glu Glu	

175	180	185	
CGT GAG TCC AAG AGT AAA AAA AGG AAC TAT GAA AAC CTC GAC CAA CTG Arg Glu Ser Lys Ser Lys Lys Arg Asn Tyr Glu Asn Leu Asp Gln Leu 190 195 200			867
TCC TAT GAC AAC AAG CGC GGA CCC AAG GCA GAG AAG GTG CTG CAG TTT Ser Tyr Asp Asn Lys Arg Gly Pro Lys Ala Glu Lys Val Leu Gln Phe 205 210 215			915
GAC CCA GGG ACC AAG AAC GTG ACG GCC CTG CTG ATG GAG GCG AAA GAG Asp Pro Gly Thr Lys Asn Val Thr Ala Leu Leu Met Glu Ala Lys Glu 220 225 230			963
CTG GAG GCC CGG GTC ATC ATC CTT TCT GCC AGC GAG GAC GAT GCT GCC Leu Glu Ala Arg Val Ile Ile Leu Ser Ala Ser Glu Asp Asp Ala Ala 235 240 245 250			1011
ACT GTA TAC CGC GCA GCC GCG ATG CTG AAC ATG ACG GGC TCC GGG TAC Thr Val Tyr Arg Ala Ala Ala Met Leu Asn Met Thr Gly Ser Gly Tyr 255 260 265			1059
GTG TGG CTG GTC GGC GAG CGC GAG ATC TCG GGG AAC GCC CTG CGC TAC Val Trp Leu Val Gly Glu Arg Glu Ile Ser Gly Asn Ala Leu Arg Tyr 270 275 280			1107
GCC CCA GAC GGC ATC CTC GGG CTG CAG CTC ATC AAC GGC AAG AAC GAG Ala Pro Asp Gly Ile Leu Gly Leu Gln Leu Ile Asn Gly Lys Asn Glu 285 290 295			1155
TCG GCC CAC ATC AGC GAC GCC GTG GGC GTG GTG GCC CAG GCC GTG CAC Ser Ala His Ile Ser Asp Ala Val Gly Val Val Ala Gln Ala Val His 300 305 310			1203
GAG CTC CTC GAG AAG GAG AAC ATC ACC GAC CCG CCG CGG GGC TGC GTG Glu Leu Leu Glu Lys Glu Asn Ile Thr Asp Pro Pro Arg Gly Cys Val 315 320 325 330			1251
GGC AAC ACC AAC ATC TGG AAG ACC GGG CCG CTC TTC AAG AGA GTG CTG Gly Asn Thr Asn Ile Trp Lys Thr Gly Pro Leu Phe Lys Arg Val Leu 335 340 345			1299
ATG TCT TCC AAG TAT GCG GAT GGG GTG ACT GGT CGC GTG GAG TTC AAT Met Ser Ser Lys Tyr Ala Asp Gly Val Thr Gly Arg Val Glu Phe Asn 350 355 360			1347
GAG GAT GGG GAC CGG AAG TTC GCC AAC TAC AGC ATC ATG AAC CTG CAG Glu Asp Gly Asp Arg Lys Phe Ala Asn Tyr Ser Ile Met Asn Leu Gln 365 370 375			1395
AAC CGC AAG CTG GTG CAA GTG GGC ATC TAC AAT GGC ACC CAC GTC ATC Asn Arg Lys Leu Val Gln Val Gly Ile Tyr Asn Gly Thr His Val Ile 380 385 390			1443
CCT AAT GAC AGG AAG ATC ATC TGG CCA GGC GGA GAG ACA GAG AAG CCT Pro Asn Asp Arg Lys Ile Ile Trp Pro Gly Gly Glu Thr Glu Lys Pro 395 400 405 410			1491
CGA GGG TAC CAG ATG TCC ACC AGA CTG AAG ATT GTG ACG ATC CAC CAG Arg Gly Tyr Gln Met Ser Thr Arg Leu Lys Ile Val Thr Ile His Gln 415 420 425			1539
GAG CCC TTC GTG TAC GTC AAG CCC ACG CTG AGT GAT GGG ACA TGC AAG Glu Pro Phe Val Tyr Val Lys Pro Thr Leu Ser Asp Gly Thr Cys Lys 430 435 440			1587
GAG GAG TTC ACA GTC AAC GGC GAC CCA GTC AAG AAG GTG ATC TGC ACC			1635

Glu	Glu	Phe	Thr	Val	Asn	Gly	Asp	Pro	Val	Lys	Lys	Val	Ile	Cys	Thr		
445						450					455						
GGG	CCC	AAC	GAC	ACG	TCG	CCG	GGC	AGC	CCC	CGC	CAC	ACG	GTG	CCT	CAG	1683	
Gly	Pro	Asn	Asp	Thr	Ser	Pro	Gly	Ser	Pro	Arg	His	Thr	Val	Pro	Gln		
460					465					470							
TGT	TGC	TAC	GGC	TTT	TGC	ATC	GAC	CTG	CTC	ATC	AAG	CTG	GCA	CGG	ACC	1731	
Cys	Cys	Tyr	Gly	Phe	Cys	Ile	Asp	Leu	Leu	Ile	Lys	Leu	Ala	Arg	Thr		
475					480				485					490			
ATG	AAC	TTC	ACC	TAC	GAG	GTG	CAC	CTG	GTG	GCA	GAT	GGC	AAG	TTC	GGC	1779	
Met	Asn	Phe	Thr	Tyr	Glu	Val	His	Leu	Val	Ala	Asp	Gly	Lys	Phe	Gly		
					495				500				505				
ACA	CAG	GAG	CGG	GTG	AAC	AAC	AGC	AAC	AAG	AAG	GAG	TGG	AAT	GGG	ATG	1827	
Thr	Gln	Glu	Arg	Val	Asn	Asn	Ser	Asn	Lys	Lys	Glu	Trp	Asn	Gly	Met		
510						515					520						
ATG	GGC	GAG	CTG	CTC	AGC	GGG	CAG	GCA	GAC	ATG	ATC	GTG	GCG	CCG	CTA	1875	
Met	Gly	Glu	Leu	Leu	Ser	Gly	Gln	Ala	Asp	Met	Ile	Val	Ala	Pro	Leu		
525						530					535						
ACC	ATA	AAC	AAC	GAG	CGC	GCG	CAG	TAC	ATC	GAG	TTT	TCC	AAG	CCC	TTC	1923	
Thr	Ile	Asn	Asn	Glu	Arg	Ala	Gln	Tyr	Ile	Glu	Ser	Lys	Pro	Phe			
540						545				550							
AAG	TAC	CAG	GGC	CTG	ACT	ATT	CTG	GTC	AAG	AAG	GAG	ATT	CCC	CGG	AGC	1971	
Lys	Tyr	Gln	Gly	Leu	Thr	Ile	Leu	Val	Lys	Lys	Glu	Ile	Pro	Arg	Ser		
555						560			565			570					
ACG	CTG	GAC	TCG	TTC	ATG	CAG	CCG	TTC	CAG	AGC	ACA	CTG	TGG	CTG	CTG	2019	
Thr	Leu	Asp	Ser	Phe	Met	Gln	Pro	Phe	Ser	Thr	Leu	Trp	Leu	Leu			
575							580					585					
GTG	GGG	CTG	TCG	GTG	CAC	GTG	GTG	GCC	GTG	ATG	CTG	TAC	CTG	CTG	GAC	2067	
Val	Gly	Leu	Ser	Val	His	Val	Val	Ala	Val	Met	Leu	Tyr	Leu	Leu	Asp		
590						595					600						
CGC	TTC	AGC	CCC	TTC	GGC	CGG	TTC	AAG	GTG	AAC	AGC	GAG	GAG	GAG	GAG	2115	
Arg	Phe	Ser	Pro	Phe	Gly	Arg	Phe	Lys	Val	Asn	Ser	Glu	Glu	Glu	Glu		
605						610					615						
GAG	GAC	GCA	CTG	ACC	CTG	TCC	TCG	GCC	ATG	TGG	TTC	TCC	TGG	GGC	GTC	2163	
Glu	Asp	Ala	Leu	Thr	Leu	Ser	Ser	Ala	Met	Trp	Phe	Ser	Trp	Gly	Val		
620						625					630						
CTG	CTC	AAC	TCC	GGC	ATC	GGG	GAA	GGC	GCC	CCC	AGA	AGC	TTC	TCA	GCG	2211	
Leu	Leu	Asn	Ser	Gly	Ile	Gly	Glu	Gly	Ala	Pro	Arg	Ser	Phe	Ser	Ala		
635						640				645			650				
CGC	ATC	CTG	GGC	ATG	GTG	TGG	GCC	GGC	TTT	GCC	ATG	ATC	ATC	GTG	GCC	2259	
Arg	Ile	Leu	Gly	Met	Val	Trp	Ala	Gly	Phe	Ala	Met	Ile	Ile	Val	Ala		
655							660					665					
TCC	TAC	ACC	GCC	AAC	CTG	GCG	GCC	TTC	CTG	GTG	CTG	GAC	CGG	CCG	GAG	2307	
Ser	Tyr	Thr	Ala	Asn	Leu	Ala	Ala	Phe	Leu	Val	Leu	Asp	Arg	Pro	Glu		
670							675					680					
GAG	CGC	ATC	ACG	GGC	ATC	AAC	GAC	CCT	CGG	CTG	AGG	AAC	CCC	TCG	GAC	2355	
Glu	Arg	Ile	Thr	Gly	Ile	Asn	Asp	Pro	Arg	Leu	Arg	Asn	Pro	Ser	Asp		
685						690					695						
AAG	TTT	ATC	TAC	GCC	ACG	GTG	AAG	CAG	AGC	TCC	GTG	GAT	ATC	TAC	TTC	2403	
Lys	Phe	Ile	Tyr	Ala	Thr	Val	Lys	Gln	Ser	Ser	Val	Asp	Ile	Tyr	Phe		
700						705					710						

CGG CGC CAG GTG GAG CTG AGC ACC ATG TAC CGG CAT ATG GAG AAG CAC Arg Arg Gln Val Glu Leu Ser Thr Met Tyr Arg His Met Glu Lys His 715 720 725 730	2451
AAC TAC GAG AGT GCG GCG GAG GCC ATC CAG GCC GTG AGA GAC AAC AAG Asn Tyr Glu Ser Ala Ala Glu Ala Ile Gln Ala Val Arg Asp Asn Lys 735 740 745	2499
CTG CAT GCC TTC ATC TGG GAC TCG GCG GTG CTG GAG TTC GAG GCC TCG Leu His Ala Phe Ile Trp Asp Ser Ala Val Leu Glu Phe Glu Ala Ser 750 755 760	2547
CAG AAG TGC GAC CTG GTG ACG ACT GGA GAG CTG TTT TTC CGC TCG GGC Gln Lys Cys Asp Leu Val Thr Thr Gly Glu Leu Phe Phe Arg Ser Gly 765 770 775	2595
TTC GGC ATA GGC ATG CGC AAA GAC AGC CCC TGG AAG CAG AAC GTC TCC Phe Gly Ile Gly Met Arg Lys Asp Ser Pro Trp Lys Gln Asn Val Ser 780 785 790	2643
CTG TCC ATC CTC AAG TCC CAC GAG AAT GGC TTC ATG GAA GAC CTG GAC Leu Ser Ile Leu Lys Ser His Glu Asn Gly Phe Met Glu Asp Leu Asp 795 800 805 810	2691
AAG ACG TGG GTT CGG TAT CAG GAA TGT GAC TCG CGC AGC AAC GCC CCT Lys Thr Trp Val Arg Tyr Gln Glu Cys Asp Ser Arg Ser Asn Ala Pro 815 820 825	2739
GCG ACC CTT ACT TTT GAG AAC ATG GCC GGG GTC TTC ATG CTG GTA GCT Ala Thr Leu Thr Phe Glu Asn Met Ala Gly Val Phe Met Leu Val Ala 830 835 840	2787
GGG GGC ATC GTG GCC GGG ATC TTC CTG ATT TTC ATC GAG ATT GCC TAC Gly Gly Ile Val Ala Gly Ile Phe Leu Ile Phe Ile Glu Ile Ala Tyr 845 850 855	2835
AAG CGG CAC AAG GAT GCT CGC CGG AAG CAG ATG CAG CTG GCC TTT GCC Lys Arg His Lys Asp Ala Arg Arg Lys Gln Met Gln Leu Ala Phe Ala 860 865 870	2883
GCC GTT AAC GTG TGG CGG AAG AAC CTG CAG GAT AGA AAG AGT GGT AGA Ala Val Asn Val Trp Arg Lys Asn Leu Gln Asp Arg Lys Ser Gly Arg 875 880 885 890	2931
GCA GAG CCT GAC CCT AAA AAG AAA GCC ACA TTT AGG GCT ATC ACC TCC Ala Glu Pro Asp Pro Lys Lys Ala Thr Phe Arg Ala Ile Thr Ser 895 900 905	2979
ACC CTG GCT TCC AGC TTC AAG AGG CGT AGG TCC TCC AAA GAC ACG CAG Thr Leu Ala Ser Ser Phe Lys Arg Arg Ser Ser Lys Asp Thr Gln 910 915 920	3027
TAC CAT CCC ACT GAT ATC ACG GGC CCG CTC AAC CTC TCA GAT CCC TCG Tyr His Pro Thr Asp Ile Thr Gly Pro Leu Asn Leu Ser Asp Pro Ser 925 930 935	3075
GTC AGC ACC GTG GTG TGAGGCCCGGG GGAGGCGCCCC ACCTGCCAG TTAGCCGGC Val Ser Thr Val Val 940	3130
CAAGGACACT GATGGGTCT GCTGCTCGGG AAGGCCTGAG GGAAGCCCAC CGGCCCCAGA	3190
GACTGCCAC CCTGGGCCTC CCGTCCGTCG GCGCGCCAC CCCGCTGCCCT GGCGGGCAGC	3250
CCCTGCTGGA CCAAGGTGCG GACCGGAGCG GCTGAGGACG GGGCAGAGCT GAGTCGGCTG	3310
GGCAGGGCCCG CAGGGCGCTC CGGCAGAGGC AGGCCCTGG GGTCTCTGAG CAGTGGGGAG	3370

CGGGGGCTAA	CTGCCCCAG	GCGGAGGGC	TTGGAGCAGA	GACGGCAGCC	CCATCCTTCC	3430
CGCAGCACCA	GCCTGAGCCA	CAGTGGGCC	CATGGCCCCA	GCTGGCTGGG	TCGCCCCCTCC	3490
TCGGGCGCCT	GCGCTCCTCT	GCAGGCTGAG	CTCCACCCCTC	CCCTCTTCTT	GCGGCACCGC	3550
CCACCAAACA	CCCCGTCTGC	CCCTTGACGC	CACACGCCGG	GGCTGGCGCT	GCCCTCCCCC	3610
ACGGCCGTCC	CTGACTTCCC	AGCTGGCAGC	GCCTCCGCC	GCCTCGGGCC	GCCTCCTCCA	3670
GAATCGAGAG	GGCTGAGCCC	CTCCTCTCCT	CGTCCGGCCT	GCAGCACAGA	AGGGGGCCTC	3730
CCCGGGGGTC	CCCGGACGCT	GGCTCGGGAC	TGTCTTCAAC	CCTGCCCTGC	ACCTTGGGCA	3790
CGGGAGAGCG	CCACCCGCC	GCCCCGCC	TCGCTCCGGG	TGCGTGACCG	GCCCGCCACC	3850
TTGTACAGAA	CCAGCACTCC	CAGGCCCGA	GCGCGTGCCT	TCCCCGTGCG	CAGCCGCGCT	3910
CTGCCCCCTCC	GTCCCCAGGG	TGCAGGCGCG	CACCGCCCAA	CCCCCACCTC	CCGGTGATATG	3970
CAGTGGTGAT	GCCTAAAGGA	ATGTCACG				3998

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 943 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Met	Ser	Thr	Met	Arg	Leu	Leu	Thr	Leu	Ala	Leu	Leu	Phe	Ser	Cys	Ser
1					5			10						15	
Val	Ala	Arg	Ala	Ala	Cys	Asp	Pro	Lys	Ile	Val	Asn	Ile	Gly	Ala	Val
					20			25				30			
Leu	Ser	Thr	Arg	Lys	His	Glu	Gln	Met	Phe	Arg	Glu	Ala	Val	Asn	Gln
					35		40				45				
Ala	Asn	Lys	Arg	His	Gly	Ser	Trp	Lys	Ile	Gln	Leu	Asn	Ala	Thr	Ser
					50		55		60						
Val	Thr	His	Lys	Pro	Asn	Ala	Ile	Gln	Met	Ala	Leu	Ser	Val	Cys	Glu
					65		70		75				80		
Asp	Leu	Ile	Ser	Ser	Gln	Val	Tyr	Ala	Ile	Leu	Val	Ser	His	Pro	Pro
					85		90				95				
Thr	Pro	Asn	Asp	His	Phe	Thr	Pro	Thr	Pro	Val	Ser	Tyr	Thr	Ala	Gly
					100		105				110				
Phe	Tyr	Arg	Ile	Pro	Val	Leu	Gly	Leu	Thr	Thr	Arg	Met	Ser	Ile	Tyr
					115		120				125				
Ser	Asp	Lys	Ser	Ile	His	Leu	Ser	Phe	Leu	Arg	Thr	Val	Pro	Pro	Tyr
					130		135				140				
Ser	His	Gln	Ser	Ser	Val	Trp	Phe	Glu	Met	Met	Arg	Val	Tyr	Ser	Trp
					145		150		155		160				
Asn	His	Ile	Ile	Leu	Leu	Val	Ser	Asp	Asp	His	Glu	Gly	Arg	Ala	Ala
					165		170				175				

Gln Lys Arg Leu Glu Thr Leu Leu Glu Glu Arg Glu Ser Lys Ser Lys
180 185 190

Lys Arg Asn Tyr Glu Asn Leu Asp Gln Leu Ser Tyr Asp Asn Lys Arg
195 200 205

Gly Pro Lys Ala Glu Lys Val Leu Gln Phe Asp Pro Gly Thr Lys Asn
210 215 220

Val Thr Ala Leu Leu Met Glu Ala Lys Glu Leu Glu Ala Arg Val Ile
225 230 235 240

Ile Leu Ser Ala Ser Glu Asp Asp Ala Ala Thr Val Tyr Arg Ala Ala
245 250 255

Ala Met Leu Asn Met Thr Gly Ser Gly Tyr Val Trp Leu Val Gly Glu
260 265 270

Arg Glu Ile Ser Gly Asn Ala Leu Arg Tyr Ala Pro Asp Gly Ile Leu
275 280 285

Gly Leu Gln Leu Ile Asn Gly Lys Asn Glu Ser Ala His Ile Ser Asp
290 295 300

Ala Val Gly Val Val Ala Gln Ala Val His Glu Leu Leu Glu Lys Glu
305 310 315 320

Asn Ile Thr Asp Pro Pro Arg Gly Cys Val Gly Asn Thr Asn Ile Trp
325 330 335

Lys Thr Gly Pro Leu Phe Lys Arg Val Leu Met Ser Ser Lys Tyr Ala
340 345 350

Asp Gly Val Thr Gly Arg Val Glu Phe Asn Glu Asp Gly Asp Arg Lys
355 360 365

Phe Ala Asn Tyr Ser Ile Met Asn Leu Gln Asn Arg Lys Leu Val Gln
370 375 380

Val Gly Ile Tyr Asn Gly Thr His Val Ile Pro Asn Asp Arg Lys Ile
385 390 395 400

Ile Trp Pro Gly Gly Glu Thr Glu Lys Pro Arg Gly Tyr Gln Met Ser
405 410 415

Thr Arg Leu Lys Ile Val Thr Ile His Gln Glu Pro Phe Val Tyr Val
420 425 430

Lys Pro Thr Leu Ser Asp Gly Thr Cys Lys Glu Glu Phe Thr Val Asn
435 440 445

Gly Asp Pro Val Lys Lys Val Ile Cys Thr Gly Pro Asn Asp Thr Ser
450 455 460

Pro Gly Ser Pro Arg His Thr Val Pro Gln Cys Cys Tyr Gly Phe Cys
465 470 475 480

Ile Asp Leu Leu Ile Lys Leu Ala Arg Thr Met Asn Phe Thr Tyr Glu
485 490 495

Val His Leu Val Ala Asp Gly Lys Phe Gly Thr Gln Glu Arg Val Asn
500 505 510

Asn Ser Asn Lys Lys Glu Trp Asn Gly Met Met Gly Glu Leu Leu Ser
515 520 525

Gly Gln Ala Asp Met Ile Val Ala Pro Leu Thr Ile Asn Asn Glu Arg

530 535 540

Ala Gln Tyr Ile Glu Phe Ser Lys Pro Phe Lys Tyr Gln Gly Leu Thr
545 550 555 560

Ile Leu Val Lys Lys Glu Ile Pro Arg Ser Thr Leu Asp Ser Phe Met
565 570 575

Gln Pro Phe Gln Ser Thr Leu Trp Leu Leu Val Gly Leu Ser Val His
580 585 590

Val Val Ala Val Met Leu Tyr Leu Leu Asp Arg Phe Ser Pro Phe Gly
595 600 605

Arg Phe Lys Val Asn Ser Glu Glu Glu Glu Asp Ala Leu Thr Leu
610 615 620

Ser Ser Ala Met Trp Phe Ser Trp Gly Val Leu Leu Asn Ser Gly Ile
625 630 635 640

Gly Glu Gly Ala Pro Arg Ser Phe Ser Ala Arg Ile Leu Gly Met Val
645 650 655

Trp Ala Gly Phe Ala Met Ile Ile Val Ala Ser Tyr Thr Ala Asn Leu
660 665 670

Ala Ala Phe Leu Val Leu Asp Arg Pro Glu Glu Arg Ile Thr Gly Ile
675 680 685

Asn Asp Pro Arg Leu Arg Asn Pro Ser Asp Lys Phe Ile Tyr Ala Thr
690 695 700

Val Lys Gln Ser Ser Val Asp Ile Tyr Phe Arg Arg Gln Val Glu Leu
705 710 715 720

Ser Thr Met Tyr Arg His Met Glu Lys His Asn Tyr Glu Ser Ala Ala
725 730 735

Glu Ala Ile Gln Ala Val Arg Asp Asn Lys Leu His Ala Phe Ile Trp
740 745 750

Asp Ser Ala Val Leu Glu Phe Glu Ala Ser Gln Lys Cys Asp Leu Val
755 760 765

Thr Thr Gly Glu Leu Phe Phe Arg Ser Gly Phe Gly Ile Gly Met Arg
770 775 780

Lys Asp Ser Pro Trp Lys Gln Asn Val Ser Leu Ser Ile Leu Lys Ser
785 790 795 800

His Glu Asn Gly Phe Met Glu Asp Leu Asp Lys Thr Trp Val Arg Tyr
805 810 815

Gln Glu Cys Asp Ser Arg Ser Asn Ala Pro Ala Thr Leu Thr Phe Glu
820 825 830

Asn Met Ala Gly Val Phe Met Leu Val Ala Gly Gly Ile Val Ala Gly
835 840 845

Ile Phe Leu Ile Phe Ile Glu Ile Ala Tyr Lys Arg His Lys Asp Ala
850 855 860

Arg Arg Lys Gln Met Gln Leu Ala Phe Ala Ala Val Asn Val Trp Arg
865 870 875 880

Lys Asn Leu Gln Asp Arg Lys Ser Gly Arg Ala Glu Pro Asp Pro Lys

885	890	895
Lys Lys Ala Thr Phe Arg Ala Ile Thr Ser Thr Leu Ala Ser Ser Phe		
900	905	910
Lys Arg Arg Arg Ser Ser Lys Asp Thr Gln Tyr His Pro Thr Asp Ile		
915	920	925
Thr Gly Pro Leu Asn Leu Ser Asp Pro Ser Val Ser Thr Val Val		
930	935	940

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3274 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 262..3255

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

CAAGCCGGGC GTTCGGAGCT GTGCCCGGCC CCGCTTCAGC ACCGCGGACA GCGCCGGCCG	60
CGTGGGGCTG AGCGCCGAGC CCCCGCGCAC GCTTCAGCCC CCCTTCCCTC GGCCGACGTC	120
CCGGGACCAC CGCTCCGGGG GAGACGTGGC GTCCGCAGCC CGCGGGGCCG GGCGAGCGCA	180
GGACGGCCCCG GAAGCCCCGC GGGGGATGCG CCGAGGGCCC CGCGTTCGCG CCGCGCAGAG	240
CCAGGGCCCGC GGCCCGAGCC C ATG AGC ACC ATG CGC CTG CTG ACG CTC GCC	291
Met Ser Thr Met Arg Leu Leu Thr Leu Ala	
1 5 10	
CTG CTG TTC TCC TGC GTC GCC CGT GCC GCG TGC GAC CCC AAG ATC	339
Leu Leu Phe Ser Cys Ser Val Ala Arg Ala Ala Cys Asp Pro Lys Ile	
15 20 25	
GTC AAC ATT GGC GCG GTG CTG AGC ACG CGG AAG CAC GAG CAG ATG TTC	387
Val Asn Ile Gly Ala Val Leu Ser Thr Arg Lys His Glu Gln Met Phe	
30 35 40	
CGC GAG GCC GTG AAC CAG GCC AAC AAG CGG CAC GGC TCC TGG AAG ATT	435
Arg Glu Ala Val Asn Gln Ala Asn Lys Arg His Gly Ser Trp Lys Ile	
45 50 55	
CAG CTC AAT GCC ACC TCC GTC ACG CAC AAG CCC AAC GCC ATC CAG ATG	483
Gln Leu Asn Ala Thr Ser Val Thr His Lys Pro Asn Ala Ile Gln Met	
60 65 70	
GCT CTG TCG GTG TGC GAG GAC CTC ATC TCC AGC CAG GTC TAC GCC ATC	531
Ala Leu Ser Val Cys Glu Asp Leu Ile Ser Ser Gln Val Tyr Ala Ile	
75 80 85 90	
CTA GTT AGC CAT CCA CCT ACC CCC AAC GAC CAC TTC ACT CCC ACC CCT	579
Leu Val Ser His Pro Pro Thr Pro Asn Asp His Phe Thr Pro Thr Pro	
95 100 105	

GTC TCC TAC ACA GCC GGC TTC TAC CGT ATA CCC GTG CTG GGG CTG ACC Val Ser Tyr Thr Ala Gly Phe Tyr Arg Ile Pro Val Leu Gly Leu Thr 110 115 120	627
ACC CGC ATG TCC ATC TAC TCG GAC AAG AGC ATC CAC CTG AGC TTC CTG Thr Arg Met Ser Ile Tyr Ser Asp Lys Ser Ile His Leu Ser Phe Leu 125 130 135	675
CGC ACC GTG CCG CCC TAC TCC CAC CAG TCC AGC GTG TGG TTT GAG ATG Arg Thr Val Pro Pro Tyr Ser His Gln Ser Ser Val Trp Phe Glu Met 140 145 150	723
ATG CGT GTC TAC AGC TGG AAC CAC ATC ATC CTG CTG GTC AGC GAC GAC Met Arg Val Tyr Ser Trp Asn His Ile Ile Leu Leu Val Ser Asp Asp 155 160 165 170	771
CAC GAG GGC CGG GCG GCT CAG AAA CGC CTG GAG ACG CTG CTG GAG GAG His Glu Gly Arg Ala Ala Gln Lys Arg Leu Glu Thr Leu Leu Glu Glu 175 180 185	819
CGT GAG TCC AAG AGT AAA AAA AGG AAC TAT GAA AAC CTC GAC CAA CTG Arg Glu Ser Lys Ser Lys Arg Asn Tyr Glu Asn Leu Asp Gln Leu 190 195 200	867
TCC TAT GAC AAC AAG CGC GGA CCC AAG GCA GAG AAG GTG CTG CAG TTT Ser Tyr Asp Asn Lys Arg Gly Pro Lys Ala Glu Lys Val Leu Gln Phe 205 210 215	915
GAC CCA GGG ACC AAG AAC GTG ACG GCG CTG CTG ATG GAG GCG AAA GAG Asp Pro Gly Thr Lys Asn Val Thr Ala Leu Leu Met Glu Ala Lys Glu 220 225 230	963
CTG GAG GCC CGG GTC ATC ATC CTT TCT GCC AGC GAG GAC GAT GCT GCC Leu Glu Ala Arg Val Ile Ile Leu Ser Ala Ser Glu Asp Asp Ala Ala 235 240 245 250	1011
ACT GTA TAC CGC GCA GCC GCG ATG CTG AAC ATG ACG GGC TCC GGG TAC Thr Val Tyr Arg Ala Ala Ala Met Leu Asn Met Thr Gly Ser Gly Tyr 255 260 265	1059
GTG TGG CTG GTC GGC GAG CGC GAG ATC TCG GGG AAC GCC CTG CGC TAC Val Trp Leu Val Gly Glu Arg Glu Ile Ser Gly Asn Ala Leu Arg Tyr 270 275 280	1107
GCC CCA GAC GGC ATC CTC GGG CTG CAG CTC ATC AAC GGC AAG AAC GAG Ala Pro Asp Gly Ile Leu Gly Leu Gln Leu Ile Asn Gly Lys Asn Glu 285 290 295	1155
TCG GCC CAC ATC AGC GAC GCC GTG GGC GTG GTG GCC CAG GCC GTG CAC Ser Ala His Ile Ser Asp Ala Val Gly Val Val Ala Gln Ala Val His 300 305 310	1203
GAG CTC CTC GAG AAG GAG AAC ATC ACC GAC CCG CCG CGG GGC TGC GTG Glu Leu Leu Glu Lys Glu Asn Ile Thr Asp Pro Pro Arg Gly Cys Val 315 320 325 330	1251
GGC AAC ACC AAC ATC TGG AAG ACC GGG CCG CTC TTC AAG AGA GTG CTG Gly Asn Thr Asn Ile Trp Lys Thr Gly Pro Leu Phe Lys Arg Val Leu 335 340 345	1299
ATG TCT TCC AAG TAT GCG GAT GGG GTG ACT GGT CGC GTG GAG TTC AAT Met Ser Ser Lys Tyr Ala Asp Gly Val Thr Gly Arg Val Glu Phe Asn 350 355 360	1347
GAG GAT GGG GAC CGG AAG TTC GCC AAC TAC AGC ATC ATG AAC CTG CAG Glu Asp Gly Asp Arg Lys Phe Ala Asn Tyr Ser Ile Met Asn Leu Gln	1395

365	370	375	
AAC CGC AAG CTG GTG CAA GTG GGC ATC TAC AAT GGC ACC CAC GTC ATC Asn Arg Lys Leu Val Gln Val Gly Ile Tyr Asn Gly Thr His Val Ile 380 385 390			1443
CCT AAT GAC AGG AAG ATC ATC TGG CCA GGC GGA GAG ACA GAG AAG CCT Pro Asn Asp Arg Lys Ile Ile Trp Pro Gly Gly Glu Thr Glu Lys Pro 395 400 405 410			1491
CGA GGG TAC CAG ATG TCC ACC AGA CTG AAG ATT GTG ACG ATC CAC CAG Arg Gly Tyr Gln Met Ser Thr Arg Leu Lys Ile Val Thr Ile His Gln 415 420 425			1539
GAG CCC TTC GTG TAC GTC AAG CCC ACG CTG AGT GAT GGG ACA TGC AAG Glu Pro Phe Val Tyr Val Lys Pro Thr Leu Ser Asp Gly Thr Cys Lys 430 435 440			1587
GAG GAG TTC ACA GTC AAC GGC GAC CCA GTC AAG AAG GTG ATC TGC ACC Glu Glu Phe Thr Val Asn Gly Asp Pro Val Lys Lys Val Ile Cys Thr 445 450 455			1635
GGG CCC AAC GAC ACG TCG CCG GGC AGC CCC CGC CAC ACG GTG CCT CAG Gly Pro Asn Asp Thr Ser Pro Gly Ser Pro Arg His Thr Val Pro Gln 460 465 470			1683
TGT TGC TAC GGC TTT TGC ATC GAC CTG CTC ATC AAG CTG GCA CGG ACC Cys Cys Tyr Gly Phe Cys Ile Asp Leu Leu Ile Lys Leu Ala Arg Thr 475 480 485 490			1731
ATG AAC TTC ACC TAC GAG GTG CAC CTG GTG GCA GAT GGC AAG TTC GGC Met Asn Phe Thr Tyr Glu Val His Leu Val Ala Asp Gly Lys Phe Gly 495 500 505			1779
ACA CAG GAG CGG GTG AAC AAC AGC AAC AAG AAG GAG TGG AAT GGG ATG Thr Gln Glu Arg Val Asn Asn Ser Asn Lys Lys Glu Trp Asn Gly Met 510 515 520			1827
ATG GGC GAG CTG CTC AGC GGG CAG GCA GAC ATG ATC GTG GCG CCG CTA Met Gly Glu Leu Leu Ser Gly Gln Ala Asp Met Ile Val Ala Pro Leu 525 530 535			1875
ACC ATA AAC AAC GAG CGC GCG CAG TAC ATC GAG TTT TCC AAG CCC TTC Thr Ile Asn Asn Glu Arg Ala Gln Tyr Ile Glu Phe Ser Lys Pro Phe 540 545 550			1923
AAG TAC CAG GGC CTG ACT ATT CTG GTC AAG AAG GAG ATT CCC CGG AGC Lys Tyr Gln Gly Leu Thr Ile Leu Val Lys Lys Glu Ile Pro Arg Ser 555 560 565 570			1971
ACG CTG GAC TCG TTC ATG CAG CCG TTC CAG AGC ACA CTG TGG CTG CTG Thr Leu Asp Ser Phe Met Gln Pro Phe Gln Ser Thr Leu Trp Leu Leu 575 580 585			2019
GTG GGG CTG TCG GTG CAC GTG GTG GCC GTG ATG CTG TAC CTG CTG GAC Val Gly Leu Ser Val His Val Val Met Leu Tyr Leu Leu Asp 590 595 600			2067
CGC TTT AGC CCC TTC GGC CGG TTC AAG GTG AAC AGC GAG GAG GAG GAG Arg Phe Ser Pro Phe Gly Arg Phe Lys Val Asn Ser Glu Glu Glu 605 610 615			2115
GAG GAC GCA CTG ACC CTG TCC TCG GCC ATG TGG TTC TCC TGG GGC GTC Glu Asp Ala Leu Thr Leu Ser Ser Ala Met Trp Phe Ser Trp Gly Val 620 625 630			2163
CTG CTC AAC TCC GGC ATC GGG GAA GGC GCC CCC AGA AGC TTC TCA GCG			2211

Leu	Leu	Asn	Ser	Gly	Ile	Gly	Glu	Gly	Ala	Pro	Arg	Ser	Phe	Ser	Ala	
635				640			645								650	
CGC	ATC	CTG	GGC	ATG	GTG	TGG	GCC	GGC	TTT	GCC	ATG	ATC	ATC	GTG	GCC	2259
Arg	Ile	Leu	Gly	Met	Val	Trp	Ala	Gly	Phe	Ala	Met	Ile	Ile	Val	Ala	
				655					660						665	
TCC	TAC	ACC	GCC	AAI	CTG	GCG	GCC	TTC	CTG	GTG	CTG	GAC	CGG	CCG	GAG	2307
Ser	Tyr	Thr	Ala	Asn	Leu	Ala	Ala	Phe	Leu	Val	Leu	Asp	Arg	Pro	Glu	
				670				675							680	
GAG	CGC	ATC	ACG	GGC	ATC	AAC	GAC	CCT	CGG	CTG	AGG	AAC	CCC	TCG	GAC	2355
Glu	Arg	Ile	Thr	Gly	Ile	Asn	Asp	Pro	Arg	Leu	Arg	Asn	Pro	Ser	Asp	
				685			690				695					
AAG	TTT	ATC	TAC	GCC	ACG	GTG	AAG	CAG	AGC	TCC	GTG	GAT	ATC	TAC	TTC	2403
Lys	Phe	Ile	Tyr	Ala	Thr	Val	Lys	Gln	Ser	Ser	Val	Asp	Ile	Tyr	Phe	
				700			705				710					
CGG	CGC	CAG	GTG	GAG	CTG	AGC	ACC	ATG	TAC	CGG	CAT	ATG	GAG	AAG	CAC	2451
Arg	Arg	Gln	Val	Glu	Leu	Ser	Thr	Met	Tyr	Arg	His	Met	Glu	Lys	His	
				715			720			725					730	
AAC	TAC	GAG	AGT	GCG	GCG	GAG	GCC	ATC	CAG	GCC	GTG	AGA	GAC	AAC	AAG	2499
Asn	Tyr	Glu	Ser	Ala	Ala	Glu	Ala	Ile	Gln	Ala	Val	Arg	Asp	Asn	Lys	
				735			740				745					
CTG	CAT	GCC	TTC	ATC	TGG	GAC	TCG	GCG	GTG	CTG	GAG	TTC	GAG	GCC	TCG	2547
Leu	His	Ala	Phe	Ile	Trp	Asp	Ser	Ala	Val	Leu	Glu	Phe	Glu	Ala	Ser	
				750			755				760					
CAG	AAG	TGC	GAC	CTG	GTG	ACG	ACT	GGA	GAG	CTG	TTT	TTC	CGC	TCG	GCG	2595
Gln	Lys	Cys	Asp	Leu	Val	Thr	Thr	Gly	Glu	Leu	Phe	Phe	Arg	Ser	Gly	
				765			770				775					
TTC	GCC	ATA	GGC	ATG	CGC	AAA	GAC	AGC	CCC	TGG	AAG	CAG	AAC	GTC	TCC	2643
Phe	Gly	Ile	Gly	Met	Arg	Lys	Asp	Ser	Pro	Trp	Lys	Gln	Asn	Val	Ser	
				780			785				790					
CTG	TCC	ATC	CTC	AAG	TCC	CAC	GAG	AAT	GGC	TTC	ATG	GAA	GAC	CTG	GAC	2691
Leu	Ser	Ile	Leu	Lys	Ser	His	Glu	Asn	Gly	Phe	Met	Glu	Asp	Leu	Asp	
				795			800			805				810		
AAG	ACG	TGG	GTT	CGG	TAT	CAG	GAA	TGT	GAC	TCG	CGC	AGC	AAC	GCC	CCT	2739
Lys	Thr	Trp	Val	Arg	Tyr	Gln	Glu	Cys	Asp	Ser	Arg	Ser	Asn	Ala	Pro	
				815			820				825					
GCG	ACC	CTT	ACT	TTT	GAG	AAC	ATG	GCC	GGG	GTC	TTC	ATG	CTG	GTA	GCT	2787
Ala	Thr	Leu	Thr	Phe	Glu	Asn	Met	Ala	Gly	Val	Phe	Met	Leu	Val	Ala	
				830			835				840					
GGG	GGC	ATC	GTG	GCC	GGG	ATC	TTC	CTG	ATT	TTC	ATC	GAG	ATT	GCC	TAC	2835
Gly	Gly	Ile	Val	Ala	Gly	Ile	Phe	Leu	Ile	Phe	Ile	Glu	Ile	Ala	Tyr	
				845			850				855					
AAG	CGG	CAC	AAG	GAT	GCT	CGC	CGG	AAG	CAG	ATG	CAG	CTG	GCC	TTT	GCC	2883
Lys	Arg	His	Lys	Asp	Ala	Arg	Arg	Lys	Gln	Met	Gln	Leu	Ala	Phe	Ala	
				860			865				870					
GCC	GTT	AAC	GTG	TGG	CGG	AAG	AAC	CTG	CAG	GAT	AGA	AAG	AGT	GGT	AGA	2931
Ala	Val	Asn	Val	Trp	Arg	Lys	Asn	Leu	Gln	Asp	Arg	Lys	Ser	Gly	Arg	
				875			880			885				890		
GCA	GAG	CCT	GAC	CCT	AAA	AAG	AAA	GCC	ACA	TTT	AGG	GCT	ATC	ACC	TCC	2979
Ala	Glu	Pro	Asp	Pro	Lys	Lys	Lys	Ala	Thr	Phe	Arg	Ala	Ile	Thr	Ser	
				895			900				905					

ACC CTG GCT TCC AGC TTC AAG AGG CGT AGG TCC TCC AAA GAC ACG CTG Thr Leu Ala Ser Ser Phe Lys Arg Arg Arg Ser Ser Lys Asp Thr Leu 910 915 920	3027
GCT CGG GAC TGT CTT CAA CCC TGC CCT GCA CCT TGG GCA CGG GAG AGC Ala Arg Asp Cys Leu Gln Pro Cys Pro Ala Pro Trp Ala Arg Glu Ser 925 930 935	3075
GCC ACC CGC CCG CCC CCG CCG CCC TCG CTC CGG GTG CGT GAC CGG CCC GCC Ala Thr Arg Pro Pro Pro Ser Leu Arg Val Arg Asp Arg Pro Ala 940 945 950	3123
ACC TTG TAC AGA ACC AGC ACT CCC AGG GCC CGA GCG CGT GCC TTC CCC Thr Leu Tyr Arg Thr Ser Thr Pro Arg Ala Arg Ala Arg Ala Phe Pro 955 960 965 970	3171
GTG CGC AGC CGC GCT CTG CCC CTC CGT CCC CAG GGT GCA GGC GCG CAC Val Arg Ser Arg Ala Leu Pro Leu Arg Pro Gln Gly Ala Gly Ala His 975 980 985	3219
CGC CCA ACC CCC ACC TCC CGG TGT ATG CAG TGG TGATGCCTAA AGGAATGTCA Arg Pro Thr Pro Thr Ser Arg Cys Met Gln Trp 990 995	3272
CG	3274

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 997 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Met Ser Thr Met Arg Leu Leu Thr Leu Ala Leu Leu Phe Ser Cys Ser 1 5 10 15
Val Ala Arg Ala Ala Cys Asp Pro Lys Ile Val Asn Ile Gly Ala Val 20 25 30
Leu Ser Thr Arg Lys His Glu Gln Met Phe Arg Glu Ala Val Asn Gln 35 40 45
Ala Asn Lys Arg His Gly Ser Trp Lys Ile Gln Leu Asn Ala Thr Ser 50 55 60
Val Thr His Lys Pro Asn Ala Ile Gln Met Ala Leu Ser Val Cys Glu 65 70 75 80
Asp Leu Ile Ser Ser Gln Val Tyr Ala Ile Leu Val Ser His Pro Pro 85 90 95
Thr Pro Asn Asp His Phe Thr Pro Val Ser Tyr Thr Ala Gly 100 105 110
Phe Tyr Arg Ile Pro Val Leu Gly Leu Thr Thr Arg Met Ser Ile Tyr 115 120 125
Ser Asp Lys Ser Ile His Leu Ser Phe Leu Arg Thr Val Pro Pro Tyr 130 135 140
Ser His Gln Ser Ser Val Trp Phe Glu Met Met Arg Val Tyr Ser Trp 145 150 155 160

Asn His Ile Ile Leu Leu Val Ser Asp Asp His Glu Gly Arg Ala Ala
165 170 175

Gln Lys Arg Leu Glu Thr Leu Leu Glu Glu Arg Glu Ser Lys Ser Lys
180 185 190

Lys Arg Asn Tyr Glu Asn Leu Asp Gln Leu Ser Tyr Asp Asn Lys Arg
195 200 205

Gly Pro Lys Ala Glu Lys Val Leu Gln Phe Asp Pro Gly Thr Lys Asn
210 215 220

Val Thr Ala Leu Leu Met Glu Ala Lys Glu Leu Glu Ala Arg Val Ile
225 230 235 240

Ile Leu Ser Ala Ser Glu Asp Asp Ala Ala Thr Val Tyr Arg Ala Ala
245 250 255

Ala Met Leu Asn Met Thr Gly Ser Gly Tyr Val Trp Leu Val Gly Glu
260 265 270

Arg Glu Ile Ser Gly Asn Ala Leu Arg Tyr Ala Pro Asp Gly Ile Leu
275 280 285

Gly Leu Gln Leu Ile Asn Gly Lys Asn Glu Ser Ala His Ile Ser Asp
290 295 300

Ala Val Gly Val Val Ala Gln Ala Val His Glu Leu Leu Glu Lys Glu
305 310 315 320

Asn Ile Thr Asp Pro Pro Arg Gly Cys Val Gly Asn Thr Asn Ile Trp
325 330 335

Lys Thr Gly Pro Leu Phe Lys Arg Val Leu Met Ser Ser Lys Tyr Ala
340 345 350

Asp Gly Val Thr Gly Arg Val Glu Phe Asn Glu Asp Gly Asp Arg Lys
355 360 365

Phe Ala Asn Tyr Ser Ile Met Asn Leu Gln Asn Arg Lys Leu Val Gln
370 375 380

Val Gly Ile Tyr Asn Gly Thr His Val Ile Pro Asn Asp Arg Lys Ile
385 390 395 400

Ile Trp Pro Gly Gly Glu Thr Glu Lys Pro Arg Gly Tyr Gln Met Ser
405 410 415

Thr Arg Leu Lys Ile Val Thr Ile His Gln Glu Pro Phe Val Tyr Val
420 425 430

Lys Pro Thr Leu Ser Asp Gly Thr Cys Lys Glu Glu Phe Thr Val Asn
435 440 445

Gly Asp Pro Val Lys Lys Val Ile Cys Thr Gly Pro Asn Asp Thr Ser
450 455 460

Pro Gly Ser Pro Arg His Thr Val Pro Gln Cys Cys Tyr Gly Phe Cys
465 470 475 480

Ile Asp Leu Leu Ile Lys Leu Ala Arg Thr Met Asn Phe Thr Tyr Glu
485 490 495

Val His Leu Val Ala Asp Gly Lys Phe Gly Thr Gln Glu Arg Val Asn
500 505 510

Asn Ser Asn Lys Lys Glu Trp Asn Gly Met Met Gly Glu Leu Leu Ser

515	520	525
Gly Gln Ala Asp Met Ile Val Ala Pro Leu Thr Ile Asn Asn Glu Arg		
530	535	540
Ala Gln Tyr Ile Glu Phe Ser Lys Pro Phe Lys Tyr Gin Gly Leu Thr		
545	550	555
Ile Leu Val Lys Lys Glu Ile Pro Arg Ser Thr Leu Asp Ser Phe Met		
565	570	575
Gln Pro Phe Gln Ser Thr Leu Trp Leu Leu Val Gly Leu Ser Val His		
580	585	590
Val Val Ala Val Met Leu Tyr Leu Leu Asp Arg Phe Ser Pro Phe Gly		
595	600	605
Arg Phe Lys Val Asn Ser Glu Glu Glu Glu Asp Ala Leu Thr Leu		
610	615	620
Ser Ser Ala Met Trp Phe Ser Trp Gly Val Leu Leu Asn Ser Gly Ile		
625	630	635
640		
Gly Glu Gly Ala Pro Arg Ser Phe Ser Ala Arg Ile Leu Gly Met Val		
645	650	655
Trp Ala Gly Phe Ala Met Ile Ile Val Ala Ser Tyr Thr Ala Asn Leu		
660	665	670
Ala Ala Phe Leu Val Leu Asp Arg Pro Glu Glu Arg Ile Thr Gly Ile		
675	680	685
Asn Asp Pro Arg Leu Arg Asn Pro Ser Asp Lys Phe Ile Tyr Ala Thr		
690	695	700
Val Lys Gln Ser Ser Val Asp Ile Tyr Phe Arg Arg Gln Val Glu Leu		
705	710	715
720		
Ser Thr Met Tyr Arg His Met Glu Lys His Asn Tyr Glu Ser Ala Ala		
725	730	735
Glu Ala Ile Gln Ala Val Arg Asp Asn Lys Leu His Ala Phe Ile Trp		
740	745	750
Asp Ser Ala Val Leu Glu Phe Glu Ala Ser Gln Lys Cys Asp Leu Val		
755	760	765
Thr Thr Gly Glu Leu Phe Phe Arg Ser Gly Phe Gly Ile Gly Met Arg		
770	775	780
Lys Asp Ser Pro Trp Lys Gln Asn Val Ser Leu Ser Ile Leu Lys Ser		
785	790	795
800		
His Glu Asn Gly Phe Met Glu Asp Leu Asp Lys Thr Trp Val Arg Tyr		
805	810	815
Gln Glu Cys Asp Ser Arg Ser Asn Ala Pro Ala Thr Leu Thr Phe Glu		
820	825	830
Asn Met Ala Gly Val Phe Met Leu Val Ala Gly Gly Ile Val Ala Gly		
835	840	845
Ile Phe Leu Ile Phe Ile Glu Ile Ala Tyr Lys Arg His Lys Asp Ala		
850	855	860
Arg Arg Lys Gln Met Gln Leu Ala Phe Ala Ala Val Asn Val Trp Arg		

865	870	875	880
Lys Asn Leu Gln Asp Arg Lys Ser Gly Arg Ala Glu Pro Asp Pro Lys			
885	890	895	
Lys Lys Ala Thr Phe Arg Ala Ile Thr Ser Thr Leu Ala Ser Ser Phe			
900	905	910	
Lys Arg Arg Arg Ser Ser Lys Asp Thr Leu Ala Arg Asp Cys Leu Gln			
915	920	925	
Pro Cys Pro Ala Pro Trp Ala Arg Glu Ser Ala Thr Arg Pro Pro Pro			
930	935	940	
Pro Ser Leu Arg Val Arg Asp Arg Pro Ala Thr Leu Tyr Arg Thr Ser			
945	950	955	960
Thr Pro Arg Ala Arg Ala Arg Ala Phe Pro Val Arg Ser Arg Ala Leu			
965	970	975	
Pro Leu Arg Pro Gln Gly Ala Gly Ala His Arg Pro Thr Pro Thr Ser			
980	985	990	
Arg Cys Met Gln Trp			
995			

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3070 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 262..3051

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

CAAGCCGGGC GTTCGGAGCT GTGCCCGGCC CCGCTTCAGC ACCGCGGACA GCGCCGGCCG	60
CGTGGGGCTG AGCGCCGAGC CCCCGCGCAC GCTTCAGGCC CCCTTCCCTC GGCCGACGTC	120
CCGGGACCGC CGCTCCGGGG GAGACGTGGC GTCCGCAGCC CGCGGGGCCG GGCGAGCGCA	180
GGACGGCCCG GAAGCCCCGC GGGGGATGCG CCGAGGGCCC CGCGTTCGCG CCGCGCAGAG	240
CCAGGCCCGC GGCCCGAGCC C ATG AGC ACC ATG CGC CTG CTG ACG CTC GCC	291
Met Ser Thr Met Arg Leu Leu Thr Leu Ala	
i 5 10	
CTG CTG TTC TCC TCC GTC GCC CGT GCC GCG TGC GAC CCC AAG ATC	339
Leu Leu Phe Ser Cys Ser Val Ala Arg Ala Ala Cys Asp Pro Lys Ile	
15 20 25	
GTC AAC ATT GGC GCG GTG CTG AGC ACG CGG AAG CAC GAG CAG ATG TTC	387
Val Asn Ile Gly Ala Val Leu Ser Thr Arg Lys His Glu Gln Met Phe	
30 35 40	
CGC GAG GCC GTG AAC CAG GCC AAC AAG CGG CAC GGC TCC TGG AAG ATT	435

Arg Glu Ala Val Asn Gln Ala Asn Lys Arg His Gly Ser Trp Lys Ile		
45	50	55
CAG CTC AAT GCG ACC TCC GTC ACG CAC AAG CCC AAC GCC ATC CAG ATG		483
Gln Leu Asn Ala Thr Ser Val Thr His Lys Pro Asn Ala Ile Gln Met		
60	65	70
GCT CTG TCG GTG TGC GAG GAC CTC ATC TCC AGC CAG GTC TAC GCC ATC		531
Ala Leu Ser Val Cys Glu Asp Leu Ile Ser Ser Gln Val Tyr Ala Ile		
75	80	85
90		
CTA GTT AGC CAT CCA CCT ACC CCC AAC GAC CAC TTC ACT CCC ACC CCT		579
Leu Val Ser His Pro Pro Thr Pro Asn Asp His Phe Thr Pro Thr Pro		
95	100	105
GTC TCC TAC ACA GCC GGC TTC TAC CGC ATA CCC GTG CTG GGG CTG ACC		627
Val Ser Tyr Thr Ala Gly Phe Tyr Arg Ile Pro Val Leu Gly Leu Thr		
110	115	120
ACC CGC ATG TCC ATC TAC TCG GAC AAG AGC ATC CAC CTG AGC TTC CTG		675
Thr Arg Met Ser Ile Tyr Ser Asp Lys Ser Ile His Leu Ser Phe Leu		
125	130	135
CGC ACC GTG CGC CCC TAC TCC CAC CAG TCC AGC GTG TGG TTT GAG ATG		723
Arg Thr Val Pro Pro Tyr Ser His Gln Ser Ser Val Trp Phe Glu Met		
140	145	150
ATG CGT GTC TAC AGC TGG AAC CAC ATC ATC CTG CTG GTC AGC GAC GAC		771
Met Arg Val Tyr Ser Trp Asn His Ile Ile Leu Leu Val Ser Asp Asp		
155	160	165
170		175
CAC GAG GGC CGG GCG GCT CAG AAA CGC CTG GAG ACG CTG CTG GAG GAG		819
His Glu Gly Arg Ala Ala Gln Lys Arg Leu Glu Thr Leu Leu Glu Glu		
175	180	185
CGT GAG TCC AAG AGT AAA AAA AGG AAC TAT GAA AAC CTC GAC CAA CTG		867
Arg Glu Ser Lys Ser Lys Arg Asn Tyr Glu Asn Leu Asp Gln Leu		
190	195	200
TCC TAT GAC AAC AAG CGC GGA CCC AAG GCA GAG AAG GTG CTG CAG TTT		915
Ser Tyr Asp Asn Lys Arg Gly Pro Lys Ala Glu Lys Val Leu Gln Phe		
205	210	215
GAC CCA GGG ACC AAG AAC GTG ACG GCC CTG CTG ATG GAG GCG AAA GAG		963
Asp Pro Gly Thr Lys Asn Val Thr Ala Leu Leu Met Glu Ala Lys Glu		
220	225	230
CTG GAG GCC CGG GTC ATC ATC CTT TCT GCC AGC GAG GAC GAT GCT GCC		1011
Leu Glu Ala Arg Val Ile Ile Leu Ser Ala Ser Glu Asp Asp Ala Ala		
235	240	245
250		
ACT GTA TAC CGC GCA GCC GCG ATG CTG AAC ATG ACG GGC AAC ACC AAC		1059
Thr Val Tyr Arg Ala Ala Ala Met Leu Asn Met Thr Gly Asn Thr Asn		
255	260	265
ATC TGG AAG ACC GGG CCG CTC TTC AAG AGA GTG CTG ATG TCT TCC AAG		1107
Ile Trp Lys Thr Gly Pro Leu Phe Lys Arg Val Leu Met Ser Ser Lys		
270	275	280
TAT GCG GAT GGG GTG ACT GGT CGC GTG GAG TTC AAT GAG GAT GGG GAC		1155
Tyr Ala Asp Gly Val Thr Gly Arg Val Glu Phe Asn Glu Asp Gly Asp		
285	290	295
CGG AAG TTC GCC AAC TAC AGC ATC ATG AAC CTG CAG AAC CGC AAG CTG		1203
Arg Lys Phe Ala Asn Tyr Ser Ile Met Asn Leu Gln Asn Arg Lys Leu		
300	305	310

GTG CAA GTG GGC ATC TAC AAT GGC ACC CAC GTC ATC CCT AAT GAC AGG Val Gln Val Gly Ile Tyr Asn Gly Thr His Val Ile Pro Asn Asp Arg 315 320 325 330	1251
AAG ATC ATC TGG CCA GGC GGA GAG ACA GAG AAG CCT CGA GGG TAC CAG Lys Ile Ile Trp Pro Gly Gly Glu Thr Glu Lys Pro Arg Gly Tyr Gln 335 340 345	1299
ATG TCC ACC AGA CTG AAG ATT GTG ACG ATC CAC CAG GAG CCC TTC GTG Met Ser Thr Arg Leu Lys Ile Val Thr Ile His Gln Glu Pro Phe Val 350 355 360	1347
TAC GTC AAG CCC ACG CTG AGT GAT GGG ACA TGC AAG GAG GAG TTC ACA Tyr Val Lys Pro Thr Leu Ser Asp Gly Thr Cys Lys Glu Glu Phe Thr 365 370 375	1395
GTC AAC GGC GAC CCA GTC AAG AAG GTG ATC TGC ACC GGG CCC AAC GAC Val Asn Gly Asp Pro Val Lys Lys Val Ile Cys Thr Gly Pro Asn Asp 380 385 390	1443
ACG TCG CCG GGC AGC CCC CGC CAC ACG GTG CCT CAG TGT TGC TAC GGC Thr Ser Pro Gly Ser Pro Arg His Thr Val Pro Gln Cys Cys Tyr Gly 395 400 405 410	1491
TTT TGC ATC GAC CTG CTC ATC AAG CTG GCA CGG ACC ATG AAC TTC ACC Phe Cys Ile Asp Leu Leu Ile Lys Leu Ala Arg Thr Met Asn Phe Thr 415 420 425	1539
TAC GAG GTG CAC CTG GTG GCA GAT GGC AAG TTC GGC ACA CAG GAG CGG Tyr Glu Val His Leu Val Ala Asp Gly Lys Phe Gly Thr Gln Glu Arg 430 435 440	1587
GTG AAC AAC AGC AAC AAG AAG GAG TGG AAT GGG ATG ATG GGC GAG CTG Val Asn Ser Asn Lys Lys Glu Trp Asn Gly Met Met Gly Glu Leu 445 450 455	1635
CTC AGC GGG CAG GCA GAC ATG ATC GTG CGG CCG CTA ACC ATA AAC AAC Leu Ser Gly Gln Ala Asp Met Ile Val Ala Pro Leu Thr Ile Asn Asn 460 465 470	1683
GAG CGC GCG CAG TAC ATC GAG TTT TCC AAG CCC TTC AAG TAC CAG GGC Glu Arg Ala Gln Tyr Ile Glu Phe Ser Lys Pro Phe Lys Tyr Gln Gly 475 480 485 490	1731
CTG ACT ATT CTG GTC AAG AAG GAG ATT CCC CGG AGC ACG CTG GAC TCG Leu Thr Ile Leu Val Lys Lys Glu Ile Pro Arg Ser Thr Leu Asp Ser 495 500 505	1779
TTC ATG CAG CCG TTC CAG AGC ACA CTG TGG CTG CTG GTG GGG CTG TCG Phe Met Gln Pro Phe Gln Ser Thr Leu Trp Leu Leu Val Gly Leu Ser 510 515 520	1827
GTG CAC GTG GTG GCC GTG ATG CTG TAS CTG CTG GAC CGC TTC AGC CCC Val His Val Val Ala Val Met Leu Tyr Leu Leu Asp Arg Phe Ser Pro 525 530 535	1875
TTC GGC CGG TTC AAG GTG AAC AGC GAG GAG GAG GAG GAC GCA CTG Phe Gly Arg Phe Lys Val Asn Ser Glu Glu Glu Glu Asp Ala Leu 540 545 550	1923
ACC CTG TCC TCG GCC ATG TGG TTC TCC TGG GGC GTC CTG CTC AAC TCC Thr Leu Ser Ser Ala Met Trp Phe Ser Trp Gly Val Leu Leu Asn Ser 555 560 565 570	1971
GGC ATC GGG GAA GGC GCC CCC AGA AGC TTC TCA GCG CGC ATC CTG GGC Gly Ile Gly Glu Gly Ala Pro Arg Ser Phe Ser Ala Arg Ile Leu Gly 575 580 585	2019

ATG GTG TGG GCC GGC TTT GCC ATG ATC ATC GTG GCC TCC TAA ACC GCC Met Val Trp Ala Gly Phe Ala Met Ile Ile Val Ala Ser Tyr Thr Ala 590 595 600	2067
AAC CTG GCG GCC TTC CTG GTG CTG GAC CGG CCG GAG GAG CGC ATC ACG Asn Leu Ala Ala Phe Leu Val Leu Asp Arg Pro Glu Glu Arg Ile Thr 605 610 615	2115
GGC ATC AAC GAC CCT CGG CTG AGG AAC CCC TCG GAC AAG TTT ATC TAC Gly Ile Asn Asp Pro Arg Leu Arg Asn Pro Ser Asp Lys Phe Ile Tyr 620 625 630	2163
GCC ACG GTG AAG CAG AGC TCC GTG GAT ATC TAC TTC CGG CGC CAG GTG Ala Thr Val Lys Gln Ser Ser Val Asp Ile Tyr Phe Arg Arg Gln Val 635 640 645 650	2211
GAG CTG AGC ACC ATG TAC CGG CAT ATG GAG AAG CAC AAC TAC GAG AGT Glu Leu Ser Thr Met Tyr Arg His Met Glu Lys His Asn Tyr Glu Ser 655 660 665	2259
GCG GCG GAG GCC ATC CAG GCC GTG AGA GAC AAC AAG CTG CAT GCC TTC Ala Ala Glu Ala Ile Gln Ala Val Arg Asp Asn Lys Leu His Ala Phe 670 675 680	2307
ATC TGG GAC TCG GCG GTG CTG GAG TTC GAG GCC TCG CAG AAG TGC GAC Ile Trp Asp Ser Ala Val Leu Glu Phe Glu Ala Ser Gln Lys Cys Asp 685 690 695	2355
CTG GTG ACG ACT GGA GAG CTG TTT TTC CGC TCG GGC TTC GGC ATA GGC Leu Val Thr Thr Gly Glu Leu Phe Phe Arg Ser Gly Phe Gly Ile Gly 700 705 710	2403
ATG CGC AAA GAC AGC CCC TGG AAG CAG AAC GTC TCC CTG TCC ATC CTC Met Arg Lys Asp Ser Pro Trp Lys Gln Asn Val Ser Leu Ser Ile Leu 715 720 725 730	2451
AAG TCC CAC GAG AAT GGC TTC ATG GAA GAC CTG GAC AAG ACG TGG GTT Lys Ser His Glu Asn Gly Phe Met Glu Asp Leu Asp Lys Thr Trp Val 735 740 745	2499
CGG TAT CAG GAA TGT GAC TCG CGC AGC AAC GCC CCT GCG ACC CTT ACT Arg Tyr Gln Glu Cys Asp Ser Arg Ser Asn Ala Pro Ala Thr Leu Thr 750 755 760	2547
TTT GAG AAC ATG GCC GGG GTC TTC ATG CTG GTA GCT GGG GGC ATC GTG Phe Glu Asn Met Ala Gly Val Phe Met Leu Val Ala Gly Gly Ile Val 765 770 775	2595
GCC GGG ATC TTC CTG ATT TTC ATC GAG ATT GCC TAC AAG CGG CAC AAG Ala Gly Ile Phe Leu Ile Phe Ile Glu Ile Ala Tyr Lys Arg His Lys 780 785 790	2643
GAT GCT CGC CGG AAG CAG ATG CAG CTG GCC TTT GCC GCC GTT AAC GTG Asp Ala Arg Arg Lys Gln Met Gln Leu Ala Phe Ala Ala Val Asn Val 795 800 805 810	2691
TGG CGG AAG AAC CTG CAG GAT AGA AAG AGT GGT AGA GCA GAG CCT GAC Trp Arg Lys Asn Leu Gln Asp Arg Lys Ser Gly Arg Ala Glu Pro Asp 815 820 825	2739
CCT AAA AAG AAA GCC ACA TTT AGG GCT ATC ACC TCC ACC CTG GCT TCC Pro Lys Lys Ala Thr Phe Arg Ala Ile Thr Ser Thr Leu Ala Ser 830 835 840	2787
AGC TTC AAG AGG CGT AGG TCC TCC AAA GAC ACG CTG GCT CGG GAC TGT Ser Phe Lys Arg Arg Arg Ser Ser Lys Asp Thr Leu Ala Arg Asp Cys 845 850 855	2835

CTT CAA CCC TGC CCT GCA CCT TGG GCA CGG GAG AGC GCC ACC CGC CCC Leu Gln Pro Cys Pro Ala Pro Trp Ala Arg Glu Ser Ala Thr Arg Pro 860 865 870	2883
CCC CCG CCC TCG CTC CGG GTG CGT GAC CGG CCC GCC ACC TTG TAC AGA Pro Pro Pro Ser Leu Arg Val Arg Asp Arg Pro Ala Thr Leu Tyr Arg 875 880 885 890	2931
ACC AGC ACT CCC AGG GCC CGA GCG CGT GCC TTC CCC GTG CGC AGC CGC Thr Ser Thr Pro Arg Ala Arg Ala Phe Pro Val Arg Ser Arg 895 900 905	2979
GCT CTG CCC CTC CGT CCC CAG GGT GCA GGC GCG CAC CGC CCA ACC CCC Ala Leu Pro Leu Arg Pro Gln Gly Ala Gly Ala His Arg Pro Thr Pro 910 915 920	3027
ACC TCC CGG TGT ATG CAG TGG TGATGCCCTAA AGGAATGTCA CG Thr Ser Arg Cys Met Gln Trp 925 930	3070

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 929 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Met Ser Thr Met Arg Leu Leu Thr Leu Ala Leu Leu Phe Ser Cys Ser 1 5 10 15
Val Ala Arg Ala Ala Cys Asp Pro Lys Ile Val Asn Ile Gly Ala Val 20 25 30
Leu Ser Thr Arg Lys His Glu Gln Met Phe Arg Glu Ala Val Asn Gln 35 40 45
Ala Asn Lys Arg His Gly Ser Trp Lys Ile Gln Leu Asn Ala Thr Ser 50 55 60
Val Thr His Lys Pro Asn Ala Ile Gln Met Ala Leu Ser Val Cys Glu 65 70 75 80
Asp Leu Ile Ser Ser Gln Val Tyr Ala Ile Leu Val Ser His Pro Pro 85 90 95
Thr Pro Asn Asp His Phe Thr Pro Thr Pro Val Ser Tyr Thr Ala Gly 100 105 110
Phe Tyr Arg Ile Pro Val Leu Gly Leu Thr Thr Arg Met Ser Ile Tyr 115 120 125
Ser Asp Lys Ser Ile His Leu Ser Phe Leu Arg Thr Val Pro Pro Tyr 130 135 140
Ser His Gln Ser Ser Val Trp Phe Glu Met Met Arg Val Tyr Ser Trp 145 150 155 160
Asn His Ile Ile Leu Leu Val Ser Asp Asp His Glu Gly Arg Ala Ala 165 170 175
Gln Lys Arg Leu Glu Thr Leu Leu Glu Glu Arg Glu Ser Lys Ser Lys 180 185 190

Lys Arg Asn Tyr Glu Asn Leu Asp Gln Leu Ser Tyr Asp Asn Lys Arg
195 200 205

Gly Pro Lys Ala Glu Lys Val Leu Gln Phe Asp Pro Gly Thr Lys Asn
210 215 220

Val Thr Ala Leu Leu Met Glu Ala Lys Glu Leu Glu Ala Arg Val Ile
225 230 235 240

Ile Leu Ser Ala Ser Glu Asp Asp Ala Ala Thr Val Tyr Arg Ala Ala
245 250 255

Ala Met Leu Asn Met Thr Gly Asn Thr Asn Ile Trp Lys Thr Gly Pro
260 265 270

Leu Phe Lys Arg Val Leu Met Ser Ser Lys Tyr Ala Asp Gly Val Thr
275 280 285

Gly Arg Val Glu Phe Asn Glu Asp Gly Asp Arg Lys Phe Ala Asn Tyr
290 295 300

Ser Ile Met Asn Leu Gln Asn Arg Lys Leu Val Gln Val Gly Ile Tyr
305 310 315 320

Asn Gly Thr His Val Ile Pro Asn Asp Arg Lys Ile Ile Trp Pro Gly
325 330 335

Gly Glu Thr Glu Lys Pro Arg Gly Tyr Gln Met Ser Thr Arg Leu Lys
340 345 350

Ile Val Thr Ile His Gln Glu Pro Phe Val Tyr Val Lys Pro Thr Leu
355 360 365

Ser Asp Gly Thr Cys Lys Glu Glu Phe Thr Val Asn Gly Asp Pro Val
370 375 380

Lys Lys Val Ile Cys Thr Gly Pro Asn Asp Thr Ser Pro Gly Ser Pro
385 390 395 400

Arg His Thr Val Pro Gln Cys Cys Tyr Gly Phe Cys Ile Asp Leu Leu
405 410 415

Ile Lys Leu Ala Arg Thr Met Asn Phe Thr Tyr Glu Val His Leu Val
420 425 430

Ala Asp Gly Lys Phe Gly Thr Gln Glu Arg Val Asn Asn Ser Asn Lys
435 440 445

Lys Glu Trp Asn Gly Met Met Gly Glu Leu Leu Ser Gly Gln Ala Asp
450 455 460

Met Ile Val Ala Pro Leu Thr Ile Asn Asn Glu Arg Ala Gln Tyr Ile
465 470 475 480

Glu Phe Ser Lys Pro Phe Lys Tyr Gln Gly Leu Thr Ile Leu Val Lys
485 490 495

Lys Glu Ile Pro Arg Ser Thr Leu Asp Ser Phe Met Gln Pro Phe Gln
500 505 510

Ser Thr Leu Trp Leu Leu Val Gly Leu Ser Val His Val Val Ala Val
515 520 525

Met Leu Tyr Leu Leu Asp Arg Phe Ser Pro Phe Gly Arg Phe Lys Val
530 535 540

Asn Ser Glu Glu Glu Glu Asp Ala Leu Thr Leu Ser Ser Ala Met

545 550 555 560
Trp Phe Ser Trp Gly Val Leu Leu Asn Ser Gly Ile Gly Glu Gly Ala
565 570 575
Pro Arg Ser Phe Ser Ala Arg Ile Leu Gly Met Val Trp Ala Gly Phe
580 585 590
Ala Met Ile Ile Val Ala Ser Tyr Thr Ala Asn Leu Ala Ala Phe Leu
595 600 605

Val Leu Asp Arg Pro Glu Glu Arg Ile Thr Gly Ile Asn Asp Pro Arg
610 615 620
Leu Arg Asn Pro Ser Asp Lys Phe Ile Tyr Ala Thr Val Lys Gln Ser
625 630 635 640
Ser Val Asp Ile Tyr Phe Arg Arg Gln Val Glu Leu Ser Thr Met Tyr
645 650 655
Arg His Met Glu Lys His Asn Tyr Glu Ser Ala Ala Glu Ala Ile Gln
660 665 670
Ala Val Arg Asp Asn Lys Leu His Ala Phe Ile Trp Asp Ser Ala Val
675 680 685
Leu Glu Phe Glu Ala Ser Gln Lys Cys Asp Leu Val Thr Thr Gly Glu
690 695 700
Leu Phe Phe Arg Ser Gly Phe Gly Ile Gly Met Arg Lys Asp Ser Pro
705 710 715 720
Trp Lys Gln Asn Val Ser Leu Ser Ile Leu Lys Ser His Glu Asn Gly
725 730 735
Phe Met Glu Asp Leu Asp Lys Thr Trp Val Arg Tyr Gln Glu Cys Asp
740 745 750
Ser Arg Ser Asn Ala Pro Ala Thr Leu Thr Phe Glu Asn Met Ala Gly
755 760 765
Val Phe Met Leu Val Ala Gly Gly Ile Val Ala Gly Ile Phe Leu Ile
770 775 780
Phe Ile Glu Ile Ala Tyr Lys Arg His Lys Asp Ala Arg Arg Lys Gln
785 790 795 800
Met Gln Leu Ala Phe Ala Ala Val Asn Val Trp Arg Lys Asn Leu Gln
805 810 815
Asp Arg Lys Ser Gly Arg Ala Glu Pro Asp Pro Lys Lys Ala Thr
820 825 830
Phe Arg Ala Ile Thr Ser Thr Leu Ala Ser Ser Phe Lys Arg Arg Arg
835 840 845
Ser Ser Lys Asp Thr Leu Ala Arg Asp Cys Leu Gln Pro Cys Pro Ala
850 855 860
Pro Trp Ala Arg Glu Ser Ala Thr Arg Pro Pro Pro Pro Ser Leu Arg
865 870 875 880
Val Arg Asp Arg Pro Ala Thr Leu Tyr Arg Thr Ser Thr Pro Arg Ala
885 890 895
Arg Ala Arg Ala Phe Pro Val Arg Ser Arg Ala Leu Pro Leu Arg Pro

900

905

910

Gln Gly Ala Gly Ala His Arg Pro Thr Pro Thr Ser Arg Cys Met Gln
915 920 925

Trp

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2326 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 3..2324

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

CC GGC CAC GTG TGG CTG GTG CCC AAC CTG GCG CTG GGC AGC ACC GAT Gly His Val Trp Leu Val Pro Asn Leu Ala Leu Gly Ser Thr Asp 1 5 10 15	47
GCG CCC CCC GCC ACC TTC CCC GTG GGC CTC ATC AGC GTC GTC ACC GAG Ala Pro Pro Ala Thr Phe Pro Val Gly Leu Ile Ser Val Val Thr Glu 20 25 30	95
AGC TGG CGC CTC AGC CTG CGC CAG AAG GTG CGC GAC GGC GTG GCC ATT Ser Trp Arg Leu Ser Leu Arg Gln Lys Val Arg Asp Gly Val Ala Ile 35 40 45	143
CTG GCC CTG GGC GCC CAC AGC TAC TGG CGC CAG CAT GGA ACC CTG CCA Leu Ala Leu Gly Ala His Ser Tyr Trp Arg Gln His Gly Thr Leu Pro 50 55 60	191
GCC CCG GCC GGG GAC TGC CGT GTT CAC CCT GGG CCC GTC AGC CCT GCC Ala Pro Ala Gly Asp Cys Arg Val His Pro Gly Pro Val Ser Pro Ala 65 70 75	239
CGG GAG GCC TTC TAC AGG CAC CTA CTG AAT GTC ACC TGG GAG GGC CGA Arg Glu Ala Phe Tyr Arg His Leu Leu Asn Val Thr Trp Glu Gly Arg 80 85 90 95	287
GAC TTC TCC TTC AGC CCT GGT GGG TAC CTG GTC CAG CCC ACC ATG GTG Asp Phe Ser Pro Gly Gly Tyr Leu Val Gln Pro Thr Met Val 100 105 110	335
GTG ATC GCC CTC AAC CGG CAC CGC CTC TGG GAG ATG GTG GGG CGC TGG Val Ile Ala Leu Asn Arg His Arg Leu Trp Glu Met Val Gly Arg Trp 115 120 125	383
GAG CAT GGC GTC STA TAC ATG AAG TAC CCC GTG TGG CCT CGC TAC AGT Glu His Gly Val Leu Tyr Met Lys Tyr Pro Val Trp Pro Arg Tyr Ser 130 135 140	431
GCC TCT CTG CAG CCT GTG GTG GAC AGT CGG CAC CTG ACG GTG GCC ACG Ala Ser Leu Gln Pro Val Val Asp Ser Arg His Leu Thr Val Ala Thr 145 150 155	479

CTG GAA GAG CGG CCC TTT GTC ATC GTG GAG AGC CCT GAC CCT GGC ACA Leu Glu Glu Arg Pro Phe Val Ile Val Glu Ser Pro Asp Pro Gly Thr 160 165 170 175	507
GGA GGC TGT GTC CCC AAC ACC GTG CCC TGC CGC AGG CAG AGC AAC CAC Gly Gly Cys Val Pro Asn Thr Val Pro Cys Arg Arg Gln Ser Asn His 180 185 190	575
ACC TTC AGC AGC GGG GAC GTG GCC CCC TAC ACC AAG CTC TGC TGT AAG Thr Phe Ser Ser Gly Asp Val Ala Pro Tyr Thr Lys Leu Cys Cys Lys 195 200 205	623
GGA TTC TGC ATC GAC ATC CTC AAG AAG CTG GCC AGA GTG GTC AAA TTC Gly Phe Cys Ile Asp Ile Leu Lys Lys Leu Ala Arg Val Val Lys Phe 210 215 220	671
TCC TAC GAC CTG TAC CTG GTG ACC AAC GGC AAG CAT GGC AAG CGG GTG Ser Tyr Asp Leu Tyr Leu Val Thr Asn Gly Lys His Gly Lys Arg Val 225 230 235	719
CGC GGC GTA TGG AAC GGC ATG ATT GGG GAG GTG TAC TAC AAG CGG GCA Arg Gly Val Trp Asn Gly Met Ile Gly Glu Val Tyr Tyr Lys Arg Ala 240 245 250 255	767
GAC ATG GCC ATC GGC TCC CTC ACC ATC AAT GAG GAA CGC TCC GAG ATC Asp Met Ala Ile Gly Ser Leu Thr Ile Asn Glu Glu Arg Ser Glu Ile 260 265 270	815
GTA GAC TTC TCT GTA CCC TTT GTG GAG ACG GGC ATC AGT GTG ATG GTG Val Asp Phe Ser Val Pro Phe Val Glu Thr Gly Ile Ser Val Met Val 275 280 285	863
GCT CGC AGC AAT GGC ACC GTC TCC CCC TCG GCC TTC TTG GAG CCA TAT Ala Arg Ser Asn Gly Thr Val Ser Pro Ser Ala Phe Leu Glu Pro Tyr 290 295 300	911
AGC CCT GCA GTG TGG GTG ATG ATG TTT GTC ATG TGC CTC ACT GTG GTG Ser Pro Ala Val Trp Val Met Met Phe Val Met Cys Leu Thr Val Val 305 310 315	959
GCC ATC ACC GTC TTC ATG TTC GAG TAC TTC AGC CCT GTC AGC TAC AAC Ala Ile Thr Val Phe Met Phe Glu Tyr Phe Ser Pro Val Ser Tyr Asn 320 325 330 335	1007
CAG AAC CTC ACC AGA GGC AAG AAG TCC GGG GGC CCA GCT TTC ACT ATC Gln Asn Leu Thr Arg Gly Lys Ser Gly Pro Ala Phe Thr Ile 340 345 350	1055
GGC AAG TCC GTG TGG CTG CTG TGG GCG CTG GTC TTC AAC AAC TCA GTG Gly Lys Ser Val Trp Leu Leu Trp Ala Leu Val Phe Asn Asn Ser Val 355 360 365	1103
CCC ATC GAG AAC CCG CGG GGC ACC ACC AGC AAG ATC ATG GTT CTG GTC Pro Ile Glu Asn Pro Arg Gly Thr Thr Ser Lys Ile Met Val Leu Val 370 375 380	1151
TGG GCC TTC TTT GCT GTC ATC TTC CTC GCC AGA TAC ACG GCC AAC CTG Trp Ala Phe Phe Ala Val Ile Phe Leu Ala Arg Tyr Thr Ala Asn Leu 385 390 395	1199
GCC GCC TTC ATG ATC CAA GAG CAA TAC ATC GAC ACT GTG TCG GGC CTG Ala Ala Phe Met Ile Gln Glu Gln Tyr Ile Asp Thr Val Ser Gly Leu 400 405 410 415	1247
AGT GAC AAG AAG TTT CAG CGG CCT CAA GAT CAG TAC CCA CCT TTC CGC Ser Asp Lys Lys Phe Gln Arg Pro Gln Asp Gln Tyr Pro Pro Phe Arg	1295

420	425	430	
TTC GGC ACG GTG CCC AAC GGC AGC ACG SAG CGG AAC ATC CGC AGT AAC Phe Gly Thr Val Pro Asn Gly Ser Thr Glu Arg Asn Ile Arg Ser Asn 435	440	445	1343
TAC CGT GAC ATG CAC ACC CAC ATG GTC AAG TTC AAC CAG CGC TCG GTG Tyr Arg Asp Met His Thr His Met Val Lys Phe Asn Gln Arg Ser Val 450	455	460	1391
GAG GAC GCG CTC ACC AGC CTC AAG ATG GGC AAG GAC GAG GGC TGC AAG Glu Asp Ala Leu Thr Ser Leu Lys Met Gly Lys Asp Glu Gly Cys Lys 465	470	475	1439
CTG GTC ACC ATT GGG TCT GGC AAG GTC TTT GCT ACC ACT GGC TAC GGC Leu Val Thr Ile Gly Ser Gly Lys Val Phe Ala Thr Thr Gly Tyr Gly 480	485	490	1487
ATC GCC ATG CAG AAG GAC TCC CAC TGG AAG CGG GCC ATA GAC CTG GCG Ile Ala Met Gln Lys Asp Ser His Trp Lys Arg Ala Ile Asp Leu Ala 500	505	510	1535
CTC TTG CAG TTC CTG GGG GAC GGA GAG ACA CAG AAA CTG GAG ACA GTG Leu Leu Gln Phe Leu Gly Asp Gly Glu Thr Gln Lys Leu Glu Thr Val 515	520	525	1583
TGG CTC TCA GGG ATC TGC CAG AAT GAG AAG AAC GAG GTG ATG AGC AGC Trp Leu Ser Gly Ile Cys Gln Asn Glu Lys Asn Glu Val Met Ser Ser 530	535	540	1631
AAG CTG GAC ATC GAC AAC ATG GGA GGC GTC TTC TAC ATG CTG CTG GTG Lys Leu Asp Ile Asp Asn Met Gly Gly Val Phe Tyr Met Leu Leu Val 545	550	555	1679
GCC ATG GGG CTG GCC CTG GTC TTC GCC TGG GAG CAC CTG GTC TAC Ala Met Gly Leu Ala Leu Leu Val Phe Ala Trp Glu His Leu Val Tyr 560	565	570	1727
TGG AAG CTG CGC CAC TCG GTG CCC AAC TCA TCC CAG CTG GAC TTC CTG Trp Lys Leu Arg His Ser Val Pro Asn Ser Ser Gln Leu Asp Phe Leu 580	585	590	1775
CTG GCT TTC AGC AGG GGC ATC TAC AGC TGC TTC AGC GGG GTG CAG AGC Leu Ala Phe Ser Arg Gly Ile Tyr Ser Cys Phe Ser Gly Val Gln Ser 595	600	605	1823
CTC GCC AGC CCA CCG CGG CAG GCC AGC CCG GAC CTC ACG GCC AGC TCG Leu Ala Ser Pro Pro Arg Gln Ala Ser Pro Asp Leu Thr Ala Ser Ser 610	615	620	1871
GCC CAG GCC AGC GTG CTC AAG ATT CTG CAG GCA GCC CGC GAC ATG GTG Ala Gln Ala Ser Val Leu Lys Ile Leu Gln Ala Ala Arg Asp Met Val 625	630	635	1919
ACC ACG GCG GGC GTA AGC AAC TCC CTG GAC CGC GCC ACT CGC ACC ATC Thr Thr Ala Gly Val Ser Asn Ser Leu Asp Arg Ala Thr Arg Thr Ile 640	645	650	1967
GAG AAT TGG GGT GGC GGC CGC CGT GCG CCC CCA CCG TCC CCC TGC CCG Glu Asn Trp Gly Gly Arg Arg Ala Pro Pro Pro Ser Pro Cys Pro 660	665	670	2015
ACC CCG CGG TCT GGC CCC AGC CCA TGC CTG CCC ACC CCC GAC CCG CCC Thr Pro Arg Ser Gly Pro Ser Pro Cys Leu Pro Thr Pro Asp Pro Pro 675	680	685	2063
CCA GAG CCG AGC CCC ACG GGC TGG GGA CCG CCA GAC GGG GGT CGC GCG 2111			

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 774 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- ii) MOLECULE TYPE: protein
- xii) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Gly His Val Trp Leu Val Pro Asn Leu Ala Leu Gly Ser Thr Asp Ala
 1 5 10 15

Pro Pro Ala Thr Phe Pro Val Gly Leu Ile Ser Val Val Thr Glu Ser
 20 25 30

Trp Arg Leu Ser Leu Arg Gln Lys Val Arg Asp Gly Val Ala Ile Leu
 35 40 45

Ala Leu Gly Ala His Ser Tyr Trp Arg Gln His Gly Thr Leu Pro Ala
 50 55 60

Pro Ala Gly Asp Cys Arg Val His Pro Gly Pro Val Ser Pro Ala Arg
 65 70 75 80

Glu Ala Phe Tyr Arg His Leu Leu Asn Val Thr Trp Glu Gly Arg Asp
 85 90 95

Phe Ser Phe Ser Pro Gly Gly Tyr Leu Val Gln Pro Thr Met Val Val
 100 105 110

Ile Ala Leu Asn Arg His Arg Leu Trp Glu Met Val Gly Arg Trp Glu
 115 120 125

His Gly Val Leu Tyr Met Lys Tyr Pro Val Trp Pro Arg Tyr Ser Ala
 130 135 140

Ser Leu Gln Pro Val Val Asp Ser Arg His Leu Thr Val Ala Thr Leu
 145 150 155 160

Glu Glu Arg Pro Phe Val Ile Val Glu Ser Pro Asp Pro Gly Thr Gly
 165 170 175

Gly Cys Val Pro Asn Thr Val Pro Cys Arg Arg Gln Ser Asn His Thr
180 185 190

Phe Ser Ser Gly Asp Val Ala Pro Tyr Thr Lys Leu Cys Cys Lys Gly
195 200 205

Phe Cys Ile Asp Ile Leu Lys Lys Leu Ala Arg Val Val Lys Phe Ser
210 215 220

Tyr Asp Leu Tyr Leu Val Thr Asn Gly Lys His Gly Lys Arg Val Arg
225 230 235 240

Gly Val Trp Asn Gly Met Ile Gly Glu Val Tyr Tyr Lys Arg Ala Asp
245 250 255

Met Ala Ile Gly Ser Leu Thr Ile Asn Glu Glu Arg Ser Glu Ile Val
260 265 270

Asp Phe Ser Val Pro Phe Val Glu Thr Gly Ile Ser Val Met Val Ala
275 280 285

Arg Ser Asn Gly Thr Val Ser Pro Ser Ala Phe Leu Glu Pro Tyr Ser
290 295 300

Pro Ala Val Trp Val Met Met Phe Val Met Cys Leu Thr Val Val Ala
305 310 315 320

Ile Thr Val Phe Met Phe Glu Tyr Phe Ser Pro Val Ser Tyr Asn Gln
325 330 335

Asn Leu Thr Arg Gly Lys Lys Ser Gly Gly Pro Ala Phe Thr Ile Gly
340 345 350

Lys Ser Val Trp Leu Leu Trp Ala Leu Val Phe Asn Asn Ser Val Pro
355 360 365

Ile Glu Asn Pro Arg Gly Thr Thr Ser Lys Ile Met Val Leu Val Trp
370 375 380

Ala Phe Phe Ala Val Ile Phe Leu Ala Arg Tyr Thr Ala Asn Leu Ala
385 390 395 400

Ala Phe Met Ile Gln Glu Gln Tyr Ile Asp Thr Val Ser Gly Leu Ser
405 410 415

Asp Lys Lys Phe Gln Arg Pro Gln Asp Gln Tyr Pro Pro Phe Arg Phe
420 425 430

Gly Thr Val Pro Asn Gly Ser Thr Glu Arg Asn Ile Arg Ser Asn Tyr
435 440 445

Arg Asp Met His Thr His Met Val Lys Phe Asn Gln Arg Ser Val Glu
450 455 460

Asp Ala Leu Thr Ser Leu Lys Met Gly Lys Asp Glu Gly Cys Lys Leu
465 470 475 480

Val Thr Ile Gly Ser Gly Lys Val Phe Ala Thr Thr Gly Tyr Gly Ile
485 490 495

Ala Met Gln Lys Asp Ser His Trp Lys Arg Ala Ile Asp Leu Ala Leu
500 505 510

Leu Gln Phe Leu Gly Asp Gly Glu Thr Gln Lys Leu Glu Thr Val Trp
515 520 525

Leu Ser Gly Ile Cys Gln Asn Glu Lys Asn Glu Val Met Ser Ser Lys
530 535 540

Ieu Asp Ile Asp Asn Met Gly Gly Val Phe Tyr Met Leu Leu Val Ala
545 550 555 560

Met Gly Leu Ala Leu Leu Val Phe Ala Trp Glu His Leu Val Tyr Trp
565 570 575

Lys Leu Arg His Ser Val Pro Asn Ser Ser Gln Leu Asp Phe Leu Leu
580 585 590

Ala Phe Ser Arg Gly Ile Tyr Ser Cys Phe Ser Gly Val Gln Ser Leu
595 600 605

Ala Ser Pro Pro Arg Gln Ala Ser Pro Asp Leu Thr Ala Ser Ser Ala
610 615 620

Gln Ala Ser Val Leu Lys Ile Leu Gln Ala Ala Arg Asp Met Val Thr
625 630 635 640

Thr Ala Gly Val Ser Asn Ser Leu Asp Arg Ala Thr Arg Thr Ile Glu
645 650 655

Asn Trp Gly Gly Arg Arg Ala Pro Pro Pro Ser Pro Cys Pro Thr
660 665 670

Pro Arg Ser Gly Pro Ser Pro Cys Leu Pro Thr Pro Asp Pro Pro Pro
675 680 685

Glu Pro Ser Pro Thr Gly Trp Gly Pro Pro Asp Gly Gly Arg Ala Ala
690 695 700

Leu Val Arg Arg Ala Pro Gln Pro Pro Gly Arg Pro Pro Thr Pro Gly
705 710 715 720

Pro Pro Leu Ser Asp Val Ser Arg Val Ser Arg Arg Pro Ala Trp Glu
725 730 735

Ala Arg Trp Pro Val Arg Thr Gly His Cys Gly Arg His Leu Ser Ala
740 745 750

Ser Glu Arg Pro Leu Ser Pro Ala Arg Cys His Tyr Ser Ser Phe Pro
755 760 765

Arg Ala Asp Arg Ser Gly
770

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3698 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: Coding Sequence
(B) LOCATION: 3...3698

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

TG GAG ATC CAG CCG CTC ACA GTT GGG GTC AAC ACC ACC AAC CCC AGC Glu Ile Gln Pro Leu Thr Val Gly Val Asn Thr Thr Asn Pro Ser 1 5 10 15	47
AGC CTC CTC ACC CAG ATC TGC GGC CTC CTG GGT GCT GCC CAC GTC CAC Ser Leu Leu Thr Gln Ile Cys Gly Leu Leu Gly Ala Ala His Val His 20 25 30	95
GGC ATT GTC TTT GAG GAC AAC GTG GAC ACC GAG GCG GTG GCC CAG ATC Gly Ile Val Phe Glu Asp Asn Val Asp Thr Glu Ala Val Ala Gln Ile 35 40 45	143
CTT GAC TTC ATC TCC TCC CAG ACC CAT GTG CCC ATC CTC AGC ATC AGC Leu Asp Phe Ile Ser Ser Gln Thr His Val Pro Ile Leu Ser Ile Ser 50 55 60	191
GGA GGC TCT GCT GTG GTC CTC ACC CCC AAG GAG CCG GGC TCC GCC TTC Gly Gly Ser Ala Val Val Leu Thr Pro Lys Glu Pro Gly Ser Ala Phe 65 70 75	239
CTG CAG CTG GGC GTG TCC CTG GAG CAG CAG CTG CAG GTG CTG TTC AAG Leu Gln Leu Gly Val Ser Leu Glu Gln Leu Gln Val Leu Phe Lys 80 85 90 95	287
GTG CTG GAA GAG TAC GAC TGG AGC GCC TTC GGC GTC ATC ACC AGC CTG Val Leu Glu Glu Tyr Asp Trp Ser Ala Phe Ala Val Ile Thr Ser Leu 100 105 110	335
CAC CCG GGC CAC GCG CTC TTC CTG GAG GGC GTG CGC GCC GTC GCC GAC His Pro Gly His Ala Leu Phe Leu Glu Gly Val Arg Ala Val Ala Asp 115 120 125	383
GCC AGC CAC GTG AGT TGG CGG CTG CTG GAC GTG GTC ACG CTG GAA CTG Ala Ser His Val Ser Trp Arg Leu Leu Asp Val Val Thr Leu Glu Leu 130 135 140	431
GAC CCG GGA GGG CCG CGC GCG CGC ACG CAG CGC CTG CTG CGC CAG CTC Asp Pro Gly Gly Pro Arg Ala Arg Thr Gln Arg Leu Leu Arg Gln Leu 145 150 155	479
GAC GCG CCC GTG TTT GTG GCC TAC TGC TCG CGC GAG GAG GCC GAG GTG Asp Ala Pro Val Phe Val Ala Tyr Cys Ser Arg Glu Glu Ala Glu Val 160 165 170 175	527
CTC TTC GCC GAG GCG GCG CAG GCC GGT CTG GTG GGG CCC GGC CAC GTG Leu Phe Ala Glu Ala Ala Gln Ala Gly Leu Val Gly Pro Gly His Val 180 185 190	575
TGG CTG GTG CCC AAC CTG GCG CTG GGC AGC ACC GAT GCG CCC CCC GCC Trp Leu Val Pro Asn Leu Ala Leu Gly Ser Thr Asp Ala Pro Pro Ala 195 200 205	623
ACC TTC CCC GTG GGC CTC ATC AGC GTC GTC ACC GAG AGC TGG CGC CTC Thr Phe Pro Val Gly Leu Ile Ser Val Val Thr Glu Ser Trp Arg Leu 210 215 220	671
AGC CTG CGC CAG AAG GTG CGC GAC GGC GTG GCC ATT CTG GCC CTG GGC Ser Leu Arg Gln Lys Val Arg Asp Gly Val Ala Ile Leu Ala Leu Gly 225 230 235	719
GCG CAC AGC TAC TGG CGC CAG CAT GGA ACC CAG AAG GGG GTG TGC CAG Ala His Ser Tyr Trp Arg Gln His Gly Thr Gln Lys Gly Val Cys Gln 240 245 250 255	767
CCC CGG CCG GGG ACT GCC GTG TTC ACC CTG GGC CGC TCA GCC CTG CCC Pro Arg Pro Gly Thr Ala Val Phe Thr Leu Gly Pro Ser Ala Leu Pro 260 265 270	815

GGG AGG CCT TCT ACA GGC ACC TAC TGA ATG TCA CCT GGG AGG GCC GAG Gly Arg Pro Ser Thr Gly Thr Tyr * Met Ser Pro Gly Arg Ala Glu 275 280 285	863
ACT TCT CCT TCA GCC CTG GTG GGT ACC TGG TCC AGC CCA CCA TGG TGG Thr Ser Pro Ser Ala Leu Val Gly Thr Trp Ser Ser Pro Pro Trp Trp 290 295 300	911
TGA TCG CCC TCA ACC GGC ACC GCC TCT GGG AGA TGG TGG GGC GCT GGG * Ser Pro Ser Thr Gly Thr Ala Ser Gly Arg Trp Trp Gly Ala Gly 305 310 315	959
AGC ATG GCG TCC TAT ACA TGA AGT ACC CCG TGT GGC CTC GCT ACA GTG Ser Met Ala Ser Tyr Thr * Ser Thr Pro Cys Gly Leu Ala Thr Val 320 325 330 335	1007
CCT CTC TGC AGC CTG TGG TGG ACA GTC GGC ACC TGA CGG TGG CCA CGC Pro Leu Cys Ser Leu Trp Trp Thr Val Gly Thr * Arg Trp Pro Arg 340 345 350	1055
TGG AAG AGC GGC CCT TTG TCA TCG TGG AGA GCC CTG ACC CTG GCA CAG Trp Lys Ser Gly Pro Leu Ser Ser Trp Arg Ala Leu Thr Leu Ala Gln 355 360 365	1103
GAG GCT GTG TCC CCA ACA CCG TGC CCT GCC GCA GGC AGA GCA ACC ACA Glu Ala Val Ser Pro Thr Pro Cys Pro Ala Ala Gly Arg Ala Thr Thr 370 375 380	1151
CCT TCA GCA GCG GGG ACG TGG CCC CCT ACA CCA AGC TCT GCT GTA AGG Pro Ser Ala Ala Gly Thr Trp Pro Pro Thr Pro Ser Ser Ala Val Arg 385 390 395	1199
GAT TCT GCA TCG ACA TCC TCA AGA AGC TGG CCA GAG TGG TCA AAT TCT Asp Ser Ala Ser Thr Ser Arg Ser Trp Pro Glu Trp Ser Asn Ser 400 405 410 415	1247
CCT ACG ACC TGT ACC TGG TGA CCA ACG GCA AGC ATG GCA AGC GGG TGC Pro Thr Thr Cys Thr Trp * Pro Thr Ala Ser Met Ala Ser Gly Cys 420 425 430	1295
GCG GCG TAT GGA ACG GCA TGA TTG GGG AGG TGT ACT ACA AGC GGG CAG Ala Ala Tyr Gly Thr Ala * Leu Gly Arg Cys Thr Thr Ser Gly Gln 435 440 445	1343
ACA TGG CCA TCG GCT CCC TCA CCA TCA ATG AGG AAC GCT CCG AGA TCG Thr Trp Pro Ser Ala Pro Ser Pro Ser Met Arg Asn Ala Pro Arg Ser 450 455 460	1391
TAG ACT TCT CTG TAC CCT TTG TGG AGA CGG GCA TCA GTG TGA TGG TGG * Thr Ser Leu Tyr Pro Leu Trp Arg Arg Ala Ser Val * Trp Trp 465 470 475	1439
CTC GCA GCA ATG GCA CCG TCT CCC CCT CGG CCT TCT TGG AGC CAT ATA Leu Ala Ala Met Ala Pro Ser Pro Pro Arg Pro Ser Trp Ser His Ile 480 485 490 495	1487
GCC CTG CAG TGT GGG TGA TGA TGT TTG TCA TGT GCC TCA CTG TGG TGG Ala Leu Gln Cys Gly * * Cys Leu Ser Cys Ala Ser Leu Trp Trp 500 505 510	1535
CCA TCA CCG TCT TCA TGT TCG AGT ACT TCA GCC CTG TCA GCT ACA ACC Pro Ser Pro Ser Ser Cys Ser Ser Thr Ser Ala Leu Ser Ala Thr Thr 515 520 525	1583
AGA ACC TCA CCA GAG GCA AGA CTT TCA CTA TCG GCA AGT CCG TGT GGC Arg Thr Ser Pro Glu Ala Arg Leu Ser Leu Ser Ala Ser Pro Cys Gly 530 535 540	1631

TGC TGT GGG CCG TGG TCT TCA ACA ACT CAG TGC CCA TCG AGA ACC CGC Cys Cys Gly Ala Thr Ser Ser Thr Thr Gln Cys Pro Ser Arg Thr Arg 545 550 555	1679
GGG GCA CCA CCT GCA AGA TCA TGG TTC TGG TCT GGG CCT TCT TTG CTG Gly Ala Pro Phe Ala Arg Ser Trp Phe Trp Ser Gly Pro Ser Leu Leu 560 565 570 575	1727
TCA TCT TCC TCG CCT GAT ACA CGG CCA ACC TGG CCG CCT TCA TGA TCC Ser Ser Ser Pro Asp Thr Arg Pro Thr Trp Pro Pro Ser * Ser 580 585 590	1775
AAG AGC AAT ACA TCG ACA CTG TGT CGG GCC TCA GTG ACA AGA AGT TTC Lys Ser Asn Thr Ser Thr Leu Cys Arg Ala Ser Val Thr Arg Ser Phe 595 600 605	1823
AGC GGC CTC AAG ATC AGT ACC CAC CTT TCC GCT TCG GCA CGG TGC CCA Ser Gly Leu Lys Ile Ser Thr His Leu Ser Ala Ser Ala Arg Cys Pro 610 615 620	1871
ACG GCA GCA CGG AGC GGA ACA TCC GCA GTA ACT ACC GTG ACA TGC ACA Thr Ala Ala Arg Ser Gly Thr Ser Ala Val Thr Thr Val Thr Cys Thr 625 630 635	1919
CCC ACA TGG TCA AGT TCA ACC AGC GCT CGG TGG AGG ACG CGC TCA CCA Pro Thr Trp Ser Ser Thr Ser Ala Arg Trp Arg Thr Arg Ser Pro 640 645 650 655	1967
GCC TCA AGA TGG GGA AGC TGG ATG CCT TCA TCT ATG ATG CTG CTG TCC Ala Ser Arg Trp Gly Ser Trp Met Pro Ser Ser Met Met Leu Leu Ser 660 665 670	2015
TCA ACT ACA TGG CAG GCA AGG ACG AGG GCT GCA AGC TGG TCA CCA TTG Ser Thr Thr Trp Gln Ala Arg Thr Arg Ala Ala Ser Trp Ser Pro Leu 675 680 685	2063
GGT CTG GCA AGG TCT TTG CTA CCA CTG GCT ACG GCA TCG CCA TGC AGA Gly Leu Ala Arg Ser Leu Leu Pro Leu Ala Thr Ala Ser Pro Cys Arg 690 695 700	2111
AGG ACT CCC ACT GGA AGC GGG CCA TAG ACC TGG CGC TCT TGC AGT TCC Arg Thr Pro Thr Gly Ser Gly Pro * Thr Trp Arg Ser Cys Ser Ser 705 710 715	2159
TGG GGG ACG GAG AGA CAC AGA AAC TGG AGA CAG TGT GGC TCT CAG GGA Trp Gly Thr Glu Arg His Arg Asn Trp Arg Gln Cys Gly Ser Gln Gly 720 725 730 735	2207
TCT GCC AGA ATG AGA AGA ACG AGG TGA TGA GCA GCA AGC TGG ACA TCG Ser Ala Arg Met Arg Arg Thr Arg * * Ala Ala Ser Trp Thr Ser 740 745 750	2255
ACA ACA TGG GAG GCG TCT TCT ACA TGC TGC TGG TGG CCA TGG GGC TGG Thr Thr Trp Glu Ala Ser Ser Thr Cys Cys Trp Trp Pro Trp Gly Trp 755 760 765	2303
CCC TGC TGG TCT TCG CCT GGG AGC ACC TGG TCT ACT GGA AGC TGC GCC Pro Cys Trp Ser Ser Pro Gly Ser Thr Trp Ser Thr Gly Ser Cys Ala 770 775 780	2351
ACT CGG TGC CCA ACT CAT CCC AGC TGG ACT TCC TGC TGG CTT TCA GCA Thr Arg Cys Pro Thr His Pro Ser Trp Thr Ser Cys Trp Leu Ser Ala 785 790 795	2399
GGG GCA TCT ACA GCT GCT TCA GCG GGG TGC AGA GCC TCG CCA GCC CAC Gly Ala Ser Thr Ala Ala Ser Ala Gly Cys Arg Ala Ser Pro Ala His 800 805 810 815	2447

CGC GGC AGG CCA GCC CGG ACC TCA CGG CCA GCT CGG CCC AGG CCA GCG Arg Gly Arg Pro Ala Arg Thr Ser Arg Pro Ala Arg Pro Arg Pro Ala 820	825	830	2485	
TGC TCA AGA TTC TGC AGG CAG CCC GCG ACA TGG TGA CCA CGG CGG GCG Cys Ser Arg Phe Cys Arg Gln Pro Ala Thr Trp * Pro Arg Arg Ala 835	840	845	2543	
TAA GCA ACT CCC TGG ACC GCG CCA CTC GCA CCA TCG AGA ATT GGG GTG * Ala Thr Pro Trp Thr Ala Pro Leu Ala Pro Ser Arg Ile Gly Val 850	855	860	2591	
GCG GCC GCC GTG CGC CCC CAC CGT CCC CCT GCC CGA CCC CGC GGT CTG Ala Ala Ala Val Arg Pro His Arg Pro Pro Ala Arg Pro Arg Gly Leu 865	870	875	2639	
GCC CCA GCC CAT GCC TGC CCA CCC CCG ACC CGC CCC CAG AGC CGA GCC Ala Pro Ala His Ala Cys Pro Pro Pro Thr Arg Pro Gln Ser Arg Ala 880	885	890	895	2687
CCA CGG GCT GGG GAC CGC CAG ACG GGG GTC GCG CGG CGC TTG TGC GCA Pro Arg Ala Gly Asp Arg Gln Thr Gly Val Ala Arg Arg Leu Cys Ala 900	905	910	2735	
GGG CTC CGC AGC CCC CGG GCC CCC CGA CGC CGG GGC CGC CCC TGT Gly Leu Arg Ser Pro Arg Ala Ala Pro Arg Arg Gly Arg Pro Cys 915	920	925	2783	
CCG ACG TCT CCC GAG TGT CGC GCC GGC CAG CCT GGG AGG CGC GGT GGC Pro Thr Ser Pro Glu Cys Arg Ala Ala Gln Pro Gly Arg Arg Gly Gly 930	935	940	2831	
CGG TGC GGA CCG GGC ACT GCG GGA GGC ACC TCT CGG CCT CGG AGC GGC Arg Cys Gly Pro Gly Thr Ala Gly Gly Thr Ser Arg Pro Pro Ser Gly 945	950	955	2879	
CCC TGT CGC CCG CGC GCT GTC ACT ACA GCT CCT TTC CTC GAG CCG ACC Pro Cys Arg Pro Arg Ala Val Thr Ala Pro Phe Leu Glu Pro Thr 960	965	970	975	2927
GAT CCG GCC CCT TCC TCC CGC TCT TCC CGG AGC CCC CGG AGC TGG Asp Pro Ala Ala Pro Ser Ser Arg Ser Ser Arg Ser Pro Arg Ser Trp 980	985	990	2975	
AGG ACC TGC CGC TGC TCG GTC CGG AGC AGC TGG CCC GGC GGG AGG CGC Arg Thr Cys Arg Cys Ser Val Arg Ser Ser Trp Pro Gly Gly Arg Pro 995	1000	1005	3023	
TGC TGA ACG CGG CCT GGG CCC GGG GCT CGC GCC CGA GTC ACG CTT CCC Cys * Thr Arg Pro Gly Pro Gly Ala Arg Ala Arg Val Thr Leu Pro 1010	1015	1020	3071	
TGC CCA GCT CCG TGG CCG AGG CCT TCG CTC GGC CCA GCT CGC TGC CGC Cys Pro Ala Pro Trp Pro Arg Pro Ser Leu Gly Pro Ala Arg Cys Pro 1025	1030	1035	3119	
CTG GGT GCA CCG GCC CCG CCT GCG CCC GCC CCG ACG GCC ACT CGG CCT Leu Gly Ala Pro Ala Pro Pro Ala Pro Thr Ala Thr Arg Pro 1040	1045	1050	1055	3167
GCA GGC GCT TGG CGC AGG CGC AGT CGA TGT GCT TGC CGA TCT ACC GGG Ala Gly Ala Trp Arg Arg Ser Arg Cys Ala Cys Arg Ser Thr Gly 1060	1065	1070	3215	
AGG CCT GCC AGG AGG GCG AGC AGG CAG GGG CCC CCG CCT GGC AGC ACA Arg Pro Ala Arg Arg Ala Ser Arg Gln Gly Pro Pro Pro Gly Ser Thr 1075	1080	1085	3263	

GAC	AGC	ACG	TCT	GCC	TGC	ACG	CCC	ACG	CCC	ACC	TGC	CAT	TGT	GCT	GGG	3311	
Asp	Ser	Thr	Ser	Ala	Cys	Thr	Pro	Thr	Pro	Thr	Cys	His	Cys	Ala	Gly		
1090				1095							1100						
GGG	CTG	TCT	GTC	CTC	ACC	TTC	CAC	CCT	GTG	ACA	GCC	ACG	GCT	CCT	GGC	3359	
Gly	Leu	Ser	Vai	Leu	Thr	Phe	His	Pro	Val	Thr	Ala	Thr	Ala	Pro	Gly		
1105				1110					1115								
TCT	CCG	GCG	CCT	GGG	GGC	CTC	TGG	GGC	ACA	GCG	GCA	GGA	CTC	TGG	GGC	3407	
Ser	Pro	Ala	Pro	Gly	Gly	Leu	Trp	Gly	Thr	Ala	Ala	Gly	Leu	Trp	Gly		
1120				1125					1130				1135				
TGG	GCA	CAG	GCT	ACA	GAG	ACA	GTG	GGG	GAC	TGG	ACG	AGA	TCA	GCA	GTG	3455	
Trp	Ala	Gln	Ala	Thr	Glu	Thr	Val	Gly	Asp	Trp	Thr	Arg	Ser	Ala	Val		
1140				1145					1150								
TAG	CCC	GTG	GGG	CGC	AAG	GCT	TCC	CGG	GAC	CCT	GCA	CCT	GGA	GAC	GGG	3503	
*	Pro	Val	Gly	Arg	Lys	Ala	Ser	Arg	Asp	Pro	Ala	Pro	Gly	Asp	Gly		
1155				1160					1165								
TCT	CCA	GTC	TGG	AGT	CAG	AAG	TGT	GAG	TTA	TCA	GCC	ACT	CAG	GCT	CCG	3551	
Ser	Pro	Val	Trp	Ser	Gln	Lys	Cys	Glu	Leu	Ser	Ala	Thr	Gln	Ala	Pro		
1170				1175					1180								
AGC	CAG	CTG	GAT	TCT	CTG	CCT	GCC	ACT	GTC	AGG	GTT	AAG	CGG	CAG	GCA	3599	
Ser	Gln	Leu	Asp	Ser	Leu	Pro	Ala	Thr	Val	Arg	Val	Lys	Arg	Gln	Ala		
1185				1190					1195								
GGA	TTG	GCC	CTT	CTC	TGG	CTT	CTA	CCA	TGA	AAT	CCT	GGC	CAT	GGC	ACC	3647	
Gly	Leu	Ala	Leu	Leu	Trp	Leu	Leu	Pro	*	Asn	Pro	Gly	His	Gly	Thr		
1200				1205					1210				1215				
CCA	GTG	ACA	GAT	GAT	GTC	TTC	CAT	GGT	CAT	CAG	TGA	CCT	CAG	CTA	GCC	3695	
Pro	Val	Thr	Asp	Asp	Val	Phe	His	Gly	His	Gln	*	Pro	Gln	Leu	Ala		
1220				1225					1230								
TCA															3698		
Ser																	

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3243 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: Coding Sequence
(B) LOCATION: 1...3243

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

GTG	GCC	TAC	TGC	TCG	CGC	GAG	GAG	GCC	GAG	GTG	CTC	TTC	GCC	GAG	GCG	48
Val	Ala	Tyr	Cys	Ser	Arg	Glu	Glu	Ala	Glu	Val	Leu	Phe	Ala	Glu	Ala	
1		5				10				15						
GCG	CAG	GCC	GGT	CTG	GTG	GGG	CCC	GGC	CAG	GTG	TGG	CTG	GTG	CCC	AAC	96
Ala	Gln	Ala	Gly	Leu	Val	Gly	Pro	Gly	His	Val	Trp	Leu	Val	Pro	Asn	
20		25				30										
CTG	GCG	CTG	GGC	AGC	ACC	GAT	GCG	CCC	CCC	GCC	ACC	TTC	CCC	GTG	GGC	144

Leu Ala Leu Gly Ser Thr Asp Ala Pro Pro Ala Thr Phe Pro Val Gly		
35	40	45
CTC ATC AGC GTC GTC ACC GAG AGC TGG CGC CTC AGC CTG CGC CAG AAG		192
Leu Ile Ser Val Val Thr Glu Ser Trp Arg Leu Ser Leu Arg Gln Lys		
50	55	60
GTG CGC GAC GGC GTG GCC ATT CTG GCC CTG GGC GCC CAC AGC TAC TGG		240
Val Arg Asp Gly Val Ala Ile Leu Ala Leu Gly Ala His Ser Tyr Trp		
65	70	75
CGC CAG CAT GGA ACC CAG AAG GGG GTG TGC CAG CCC CGG CCG GGG ACT		288
Arg Gln His Gly Thr Gln Lys Gly Val Cys Gln Pro Arg Pro Gly Thr		
85	90	95
GCC GTG TTC ACC CTG GGC CCG TCA GCC CTG CCC GGG AGG CCT TCT ACA		336
Ala Val Phe Thr Leu Gly Pro Ser Ala Leu Pro Gly Arg Pro Ser Thr		
100	105	110
GGC ACC TAC TGA ATG TCA CCT GGG AGG GCC GAG ACT TCT CCT TCA GCC		384
Gly Thr Tyr * Met Ser Pro Gly Arg Ala Glu Thr Ser Pro Ser Ala		
115	120	125
CTG GTG GGT ACC TGG TCC AGC CCA CCA TGG TGG TGA TCG CCC TCA ACC		432
Leu Val Gly Thr Trp Ser Ser Pro Pro Trp Trp * Ser Pro Ser Thr		
130	135	140
GGC ACC GCC TCT GGG AGA TGG TGG GGC GCT GGG AGC ATG GCG TCC TAT		480
Gly Thr Ala Ser Gly Arg Trp Trp Gly Ala Gly Ser Met Ala Ser Tyr		
145	150	155
160		
ACA TGA AGT ACC CCG TGT GGC CTC GCT ACA GTG CCT CTC TGC AGC CTG		528
Thr * Ser Thr Pro Cys Gly Leu Ala Thr Val Pro Leu Cys Ser Leu		
165	170	175
TGG TGG ACA GTC GGC ACC TGA CGG TGG CCA CGC TGG AAG AGC GGC CCT		576
Trp Trp Thr Val Gly Thr * Arg Trp Pro Arg Trp Lys Ser Gly Pro		
180	185	190
TTG TCA TCG TGG AGA GCC CTG ACC CTG GCA CAG GAG GCT GTG TCC CCA		624
Leu Ser Ser Trp Arg Ala Leu Thr Leu Ala Gln Glu Ala Val Ser Pro		
195	200	205
ACA CCG TGC CCT GCC GCA GGC AGA GCA ACC ACA CCT TCA GCA GCG GGG		672
Thr Pro Cys Pro Ala Ala Gly Arg Ala Thr Thr Pro Ser Ala Ala Gly		
210	215	220
ACG TGG CCC CCT ACA CCA AGC TCT GCT GTA AGG GAT TCT GCA TCG ACA		720
Thr Trp Pro Pro Thr Pro Ser Ser Ala Val Arg Asp Ser Ala Ser Thr		
225	230	235
240		
TCC TCA AGA AGC TGG CCA GAG TGG TCA AAT TCT CCT ACG ACC TGT ACC		768
Ser Ser Arg Ser Trp Pro Glu Trp Ser Asn Ser Pro Thr Thr Cys Thr		
245	250	255
TGG TGA CCA ACG GCA AGC ATG GCA AGC GGG TGC GCG GCG TAT GGA ACG		816
Trp * Pro Thr Ala Ser Met Ala Ser Gly Cys Ala Ala Tyr Gly Thr		
260	265	270
GCA TGA TTG GGG AGG TGT ACT ACA AGC GGG CAG ACA TGG CCA TCG GCT		864
Ala * Leu Gly Arg Cys Thr Thr Ser Gly Gln Thr Trp Pro Ser Ala		
275	280	285
CCC TCA CCA TCA ATG AGG AAC GCT CCG AGA TCG TAG ACT TCT CTG TAC		912
Pro Ser Pro Ser Met Arg Asn Ala Pro Arg Ser * Thr Ser Leu Tyr		
290	295	300

CCT TTG TGG AGA CGG GCA TCA GTG TGA TGG TGG CTC GCA GCA ATG GCA	960
Pro Leu Trp Arg Arg Ala Ser Val * Trp Trp Leu Ala Ala Met Ala	
305 311 315 320	
CCG TCT CCC CCT CAG CCT TCT TGG AGC CAT ATA GCC CTG CAG TGT GGG	1008
Pro Ser Pro Pro Arg Pro Ser Trp Ser His Ile Ala Leu Gln Cys Gly	
325 330 335	
TGA TGA TGT TTG TCA TGT GCC TCA CTG TGG TGG CCA TCA CCG TCT TCA	1056
* * Cys Leu Ser Cys Ala Ser Leu Trp Trp Pro Ser Pro Ser Ser	
340 345 350	
TGT TCG AGT ACT TCA GCT CTG TCA GCT ACA ACC AGA ACC TCA CCA GAG	1104
Cys Ser Ser Thr Ser Ala Leu Ser Ala Thr Thr Arg Thr Ser Pro Glu	
355 360 365	
GCA AGA AGT CCG GGG GCC CAG CTT TCA CTA TCG GCA AGT CCG TGT GGC	1152
Ala Arg Ser Pro Gly Ala Gln Leu Ser Leu Ser Ala Ser Pro Cys Gly	
370 375 380	
TGC TGT GGG CGC TGG TCT TCA ACA ACT CAG TGC CCA TCG AGA ACC CGC	1200
Cys Cys Gly Arg Trp Ser Ser Thr Thr Gln Cys Pro Ser Arg Thr Arg	
385 390 395 400	
GGG GCA CCA CCA GCA AGA TCA TGG TTC TGG TCT GGG CCT TCT TTG CTG	1248
Gly Ala Pro Pro Ala Arg Ser Trp Phe Trp Ser Gly Pro Ser Leu Leu	
405 410 415	
TCA TCT TCC TCG CCA GAT ACA CGG CCA ACC TGG CCG CCT TCA TGA TCC	1296
Ser Ser Ser Pro Asp Thr Arg Pro Thr Trp Pro Pro Ser * Ser	
420 425 430	
AAG AGC AAT ACA TCG ACA CTG TGT CGG GCC TCA GTG ACA AGA AGT TTC	1344
Lys Ser Asn Thr Ser Thr Leu Cys Arg Ala Ser Val Thr Arg Ser Phe	
435 440 445	
AGC GGC CTC AAG ATC AGT ACC CAC CTT TCC GCT TCG GCA CGG TGC CCA	1392
Ser Gly Leu Lys Ile Ser Thr His Leu Ser Ala Ser Ala Arg Cys Pro	
450 455 460	
ACG GCA GCA CGG AGC GGA ACA TCC GCA GTA ACT ACC GTG ACA TGC ACA	1440
Thr Ala Ala Arg Ser Gly Thr Ser Ala Val Thr Thr Val Thr Cys Thr	
465 470 475 480 485 490 495	
CCC ACA TGG TCA AGT TCA ACC AGC GCT CGG TGG AGG ACG CGC TCA CCA	1488
Pro Thr Trp Ser Ser Thr Ser Ala Arg Trp Arg Thr Arg Ser Pro	
495	
GCC TCA AGA TGG GCT CTG AGG CTC AGC CTG TCC CCA GGA AGC TGG ATG	1536
Ala Ser Arg Trp Ala Leu Arg Leu Ser Leu Ser Pro Gly Ser Trp Met	
500 505 510	
CCT TCA TCT ATG ATG CTG CTG TCC TCA ACT ACA TGG CAG GCA AGG ACG	1584
Pro Ser Ser Met Met Leu Leu Ser Ser Thr Thr Trp Gln Ala Arg Thr	
515 520 525	
AGG GCT GCA AGC TGG TCA CCA TTG GGT CTG GCA AGG TCT TTG CTA CCA	1632
Arg Ala Ala Ser Trp Ser Pro Leu Gly Leu Ala Arg Ser Leu Leu Pro	
530 535 540	
CTG GCT ACG GCA TCG CCA TGC AGA AGG ACT CCC ACT GGA AGC GGG CCA	1680
Leu Ala Thr Ala Ser Pro Cys Arg Arg Thr Pro Thr Gly Ser Gly Pro	
545 550 555 560	
TAG ACC TGG CGC TCT TGC AGT TCC TGG GGG ACG GAG AGA CAC AGA AAC	1728
* Thr Trp Arg Ser Cys Ser Ser Trp Gly Thr Glu Arg His Arg Asn	
565 570 575	

TGG AGA CAG TGT GGC TCT CAG GGA TCT GCC AGA ATG AGA AGA ACG AGG	1776
Trp Arg Gln Cys Gly Ser Gln Gly Ser Ala Arg Met Arg Arg Thr Arg	
580 585 590	
TGA TGA GCA GCA AGC TGG ACA TCG ACA ACA TGG GAG GCG TCT TCT ACA	1824
* * Ala Ala Ser Trp Thr Ser Thr Trp Glu Ala Ser Ser Thr	
595 600 605	
TGC TGC TGG TGG CCA TGG GGC TGG CCC TGC TGG TCT TCG CCT GGG AGC	1872
Cys Cys Trp Trp Pro Trp Gly Trp Pro Cys Trp Ser Ser Pro Gly Ser	
610 615 620	
ACC TGG TCT ACT GGA AGC TGC GCC ACT CGG TGC CCA ACT CAT CCC AGC	1920
Thr Trp Ser Thr Gly Ser Cys Ala Thr Arg Cys Pro Thr His Pro Ser	
625 630 635 640	
TGG ACT TCC TGC TGG CTT TCA GCA GGG GCA TCT ACA GCT GCT TCA GCG	1968
Trp Thr Ser Cys Trp Leu Ser Ala Gly Ala Ser Thr Ala Ala Ser Ala	
645 650 655	
GGG TGC AGA GCC TCG CCA GCC CAC CGC GGC AGG CCA GCC CGG ACC TCA	2016
Gly Cys Arg Ala Ser Pro Ala His Arg Gly Arg Pro Ala Arg Thr Ser	
660 665 670	
CGG CCA GCT CGG CCC AGG CCA GCG TGC TCA AGA TTC TGC AGG CAG CCC	2064
Arg Pro Ala Arg Pro Arg Pro Ala Cys Ser Arg Phe Cys Arg Gln Pro	
675 680 685	
GCG ACA TGG TGA CCA CGG CGG GCG TAA GCA ACT CCC TGG ACC GCG CCA	2112
Ala Thr Trp * Pro Arg Arg Ala * Ala Thr Pro Trp Thr Ala Pro	
690 695 700	
CTC GCA CCA TCG AGA ATT GGG GTG GCG GCC GCC GTG CGC CCC CAC CGT	2160
Leu Ala Pro Ser Arg Ile Gly Val Ala Ala Ala Val Arg Pro His Arg	
705 710 715 720	
CCC CCT GCC CGA CCC CGC GGT CTG GCC CCA GCC CAT GCC TGC CCA CCC	2208
Pro Pro Ala Arg Pro Arg Gly Leu Ala Pro Ala His Ala Cys Pro Pro	
725 730 735	
CCG ACC CGC CCC CAG AGC CGA GCC CCA CGG GCT GGG GAC CGC CAG ACG	2256
Pro Thr Arg Pro Gln Ser Arg Ala Pro Arg Ala Gly Asp Arg Gln Thr	
740 745 750	
GGG GTC GCG CGG CGC TTG TGC GCA GGG CTC CGC AGC CCC CGG GCC GCC	2304
Gly Val Ala Arg Arg Leu Cys Ala Gly Leu Arg Ser Pro Arg Ala Ala	
755 760 765	
CCC CGA CGC CGG GGC CGC CCC TGT CCG ACG TCT CCC GAG TGT CGC GCC	2352
Pro Arg Arg Arg Gly Arg Pro Cys Pro Thr Ser Pro Glu Cys Arg Ala	
770 775 780	
GCC CAG CCT GGG AGG CGC GGT GGC CGG TGC GGA CCG GGC ACT GCG GGA	2400
Ala Gln Pro Gly Arg Arg Gly Gly Arg Cys Gly Pro Gly Thr Ala Gly	
785 790 795 800	
GGC ACC TCT CGG CCT CCG AGC GGC CCC TGT CGC CCG CGC GCT GTC ACT	2448
Gly Thr Ser Arg Pro Pro Ser Gly Pro Cys Arg Pro Arg Ala Val Thr	
805 810 815	
ACA GCT CCT TTC CTC GAG CCG ACC GAT CCG GCC CCT TCC TCC CGC	2496
Thr Ala Pro Phe Leu Glu Pro Thr Asp Pro Ala Ala Pro Ser Ser Arg	
820 825 830	
TCT TCC CGG AGC CCC CGG AGC TGG AGG ACC TGC CGC TGC TCG GTC CGG	2544
Ser Ser Arg Ser Pro Arg Ser Trp Arg Thr Cys Arg Cys Ser Val Arg	
835 840 845	

AGC AGC TGG CCC GGC GGG AGG CCC TGC TGA ACG CGG CCT GGG CCC GGG Ser Ser Trp Pro Gly Gly Arg Pro Cys * Thr Arg Pro Gly Pro Gly	2592
850 855 860	
GCT CGC GCC CGA GTC ACG CTT CCC TGC CCA GCT CGG TGG CGG AGG CCT Ala Arg Ala Arg Val Thr Leu Pro Cys Pro Ala Pro Trp Pro Arg Pro	2640
865 870 875 880	
TCG CTC GGC CCA GCT CGC TGC CCG CTG GGT GCA CGG GCC CCG CCT GCG Ser Leu Gly Pro Ala Arg Cys Pro Leu Gly Ala Pro Ala Pro Pro Ala	2688
885 890 895	
CCC GCC CCG ACG GCC ACT CGG CCT GCA GGC GCT TGG CGC AGG CGC AGT Pro Ala Pro Thr Ala Thr Arg Pro Ala Gly Ala Trp Arg Arg Arg Ser	2736
900 905 910	
CGA TGT GCT TGC CGA TCT ACC GGG AGG CCT GCC AGG AGG GCG AGC AGG Arg Cys Ala Cys Arg Ser Thr Gly Arg Pro Ala Arg Arg Ala Ser Arg	2784
915 920 925	
CAG GGG CCC CCG CCT GGC AGC ACA GAC AGC ACG TCT GCC TGC ACG CCC Gln Gly Pro Pro Pro Gly Ser Thr Asp Ser Thr Ser Ala Cys Thr Pro	2832
930 935 940	
ACG CCC ACC TGC CAT TGT GCT GGG GGG CTG TCT GTC CTC ACC TTC CAC Thr Pro Thr Cys His Cys Ala Gly Gly Leu Ser Val Leu Thr Phe His	2880
945 950 955 960	
CCT GTG ACA GCC ACG GCT CCT GGC TCT CCG GCG CCT GGG GGC CTC TGG Pro Val Thr Ala Thr Ala Pro Gly Ser Pro Ala Pro Gly Gly Leu Trp	2928
965 970 975	
GGC ACA GCG GCA GGA CTC TGG GGC TGG GCA CAG GCT ACA GAG ACA GTG Gly Thr Ala Ala Gly Leu Trp Gly Trp Ala Gln Ala Thr Glu Thr Val	2976
980 985 990	
GGG GAC TGG ACG AGA TCA GCA GTG TAG CCC GTG GGA CGC AAG GCT TCC Gly Asp Trp Thr Arg Ser Ala Val * Pro Val Gly Arg Lys Ala Ser	3024
995 1000 1005	
CGG GAC CCT GCA CCT GGA GAC GGA TCT CCA GTC TGG AGT CAG AAG TGT Arg Asp Pro Ala Pro Gly Asp Gly Ser Pro Val Trp Ser Gln Lys Cys	3072
1010 1015 1020	
GAG TTA TCA GCC ACT CAG GCT CCG AGC CAG CTG GAT TCT CTG CCT GCC Glu Leu Ser Ala Thr Gln Ala Pro Ser Gln Leu Asp Ser Leu Pro Ala	3120
1025 1030 1035 1040	
ACT GTC AGG GTT AAG CGG CAG GCA GGA TTG GCC CTT CTC TGG CTT CTA Thr Val Arg Val Lys Arg Gln Ala Gly Leu Ala Leu Leu Trp Leu Leu	3168
1045 1050 1055	
CCA TGA AAT CCT GGC CAT GGC ACC CCA GTG ACA GAT GAT GTC TTC CAT Pro * Asn Pro Gly His Gly Thr Pro Val Thr Asp Asp Val Phe His	3216
1060 1065 1070	
GGT CAT CAG TGA CCT CAG CTA GCC TCA Gly His Gln * Pro Gln Leu Ala Ser	3243
1075 1080	

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4092 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both

(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 189..3923

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

CCCTTAATAA GATTTCACNAC GTACACTCGA GCCATCGCGA GTGTCTTGA GCCGCGGGTG	60
ACGGTGGCTC TCGCTGCTCG CGCCCGCTCC TCCCGCGGGG GGAGCCTGAT GCCACGTTCC	120
CTATGAATTA TTTATCGCCG GCCTAAAAAT ACCCCGAACT TCACAGCCCG AGTGACCCTC	180
CGGTGGAC ATG GGT GGG GCC CTG GGG CCG GCC CTG TTG CTC ACC TCG CTC Met Gly Gly Ala Leu Gly Pro Ala Leu Leu Leu Thr Ser Leu	230
1 5 10	
TTC GGT GCC TGG GCA GGG CTG GGT CCG GGG CAG GGC GAG CAG GGC ATG Phe Gly Ala Trp Ala Gly Leu Gly Pro Gly Gln Gly Glu Gln Gly Met	278
15 20 25 30	
ACG GTG GCC GTG GTG TTT AGC AGC TCA GGG CCG CCC CAG GCC CAG TTC Thr Val Ala Val Phe Ser Ser Gly Pro Pro Gln Ala Gln Phe	326
35 40 45	
CGT GTC CGC CTC ACC CCC CAG AGC TTC CTG GAC CTA CCC CTG GAG ATC Arg Val Arg Leu Thr Pro Gln Ser Phe Leu Asp Leu Pro Leu Glu Ile	374
50 55 60	
CAG CCG CTC ACA GTT GGG GTC AAC ACC ACC AAC CCC AGC AGC CTC CTC Gln Pro Leu Thr Val Gly Val Asn Thr Thr Asn Pro Ser Ser Leu Leu	422
65 70 75	
ACC CAG ATC TGC GGC CTC CTG GGT GCT GCC CAC GTC CAC GGC ATT GTC Thr Gln Ile Cys Gly Leu Leu Gly Ala Ala His Val His Gly Ile Val	470
80 85 90	
TTT GAG GAC AAC GTG GAC ACC GAG GCG GTG GCC CAG ATC CTT GAC TTC Phe Glu Asp Asn Val Asp Thr Glu Ala Val Ala Gln Ile Leu Asp Phe	518
95 100 105 110	
ATC TCC TCC CAG ACC CAT GTG CCC ATC CTC AGC ATC AGC GGA GGC TCT Ile Ser Ser Gln Thr His Val Pro Ile Leu Ser Ile Ser Gly Gly Ser	566
115 120 125	
GCT GTG GTC CTC ACC CCC AAG GAG CCG GGC TCC GCC TTC CTG CAG CTG Ala Val Val Leu Thr Pro Lys Glu Pro Gly Ser Ala Phe Leu Gln Leu	614
130 135 140	
GGC GTG TCC CTG GAG CAG CAG CTG CAG GTG CTG TTC AAG GTG CTG GAA Gly Val Ser Leu Glu Gln Gln Leu Gln Val Leu Phe Lys Val Leu Glu	662
145 150 155	
GAG TAC GAC TGG AGC GCC TTC GCC GTC ATC ACC AGC CTG CAC CCG GGC Glu Tyr Asp Trp Ser Ala Phe Ala Val Ile Thr Ser Leu His Pro GLY	710
160 165 170	
CAC GCG CTC TTC CTG GAG GGC GTG CGC GCC GTC GCC GAC GGC AGC CAC His Ala Leu Phe Leu Glu Gly Val Arg Ala Val Ala Asp Ala Ser His	758
175 180 185 190	
GTG AGT TGG CGG CTG CTG GAC GTG GTC ACG CTG GAA CTG GAC CCG GGA	806

Val Ser Trp Arg Leu Leu Asp Val Val Thr Leu Glu Leu Asp Pro Gly		
195	200	205
Gly Pro Arg Ala Arg Thr Gln Arg Leu Leu Arg Gln Leu Asp Ala Pro		
210	215	220
GTG TTT GTG GCC TAC TGC TCG CGC GAG GAG GCC GAG GTG CTC TTC GCC		854
Val Phe Val Ala Tyr Cys Ser Arg Glu Glu Ala Glu Val Leu Phe Ala		
225	230	235
GAG GCG GCG CAG GCC GGT CTG GTG GGG CCC GGC CAC GTG TGG CTG GTG		950
Glu Ala Ala Gln Ala Gly Leu Val Gly Pro Gly His Val Trp Leu Val		
240	245	250
CCC AAC CTG GCG CTG GGC AGC ACC GAT GCG CCC CCC GCC ACC TTC CCC		998
Pro Asn Leu Ala Leu Gly Ser Thr Asp Ala Pro Pro Ala Thr Phe Pro		
255	260	265
GTG GGC CTC ATC AGC GTC GTC ACC GAG AGC TGG CGC CTC AGC CTG CGC		1046
Val Gly Leu Ile Ser Val Val Thr Glu Ser Trp Arg Leu Ser Leu Arg		
275	280	285
CAG AAG GTG CGC GAC GGC GTG GCC ATT CTG GCC CTG GGC GCC CAC AGC		1094
Gln Lys Val Arg Asp Gly Val Ala Ile Leu Ala Leu Gly Ala His Ser		
290	295	300
TAC TGG CGC CAG CAT GGA ACC CTG CCA GCC CCG GCC GGG GAC TGC CGT		1142
Tyr Trp Arg Gln His Gly Thr Leu Pro Ala Pro Gly Asp Cys Arg		
305	310	315
GTT CAC CCT GGG CCC GTC AGC CCT GCC CGG GAG GCC TTC TAC AGG CAC		1190
Val His Pro Gly Pro Val Ser Pro Ala Arg Glu Ala Phe Tyr Arg His		
320	325	330
CTA CTG AAT GTC ACC TGG GAG GGC CGA GAC TTC TCC TTC AGC CCT GGT		1238
Leu Leu Asn Val Thr Trp Glu Gly Arg Asp Phe Ser Phe Ser Pro Gly		
335	340	345
350		
GGG TAC CTG GTC CAG CCC ACC ATG GTG GTG ATC GCC CTC AAC CGG CAC		1286
Gly Tyr Leu Val Gln Pro Thr Met Val Val Ile Ala Leu Asn Arg His		
355	360	365
CGC CTC TGG GAG ATG GTG GGG CGC TGG GAG CAT GGC GTC CTA TAC ATG		1334
Arg Leu Trp Glu Met Val Gly Arg Trp Glu His Gly Val Leu Tyr Met		
370	375	380
AAG TAC CCC GTG TGG CCT CGC TAC AGT GCC TCT CTG CAG CCT GTG GTG		1382
Lys Tyr Pro Val Trp Pro Arg Tyr Ser Ala Ser Leu Gln Pro Val Val		
385	390	395
GAC AGT CGG CAC CTG ACG GTG GCC ACG CTG GAA GAG CGG CCC TTT GTC		1430
Asp Ser Arg His Leu Thr Val Ala Thr Leu Glu Glu Arg Pro Phe Val		
400	405	410
ATC GTG GAG AGC CCT GAC CCT GGC ACA GGA GGC TGT GTC CCC AAC ACC		1478
Ile Val Glu Ser Pro Asp Pro Gly Thr Gly Gly Cys Val Pro Asn Thr		
415	420	425
430		
GTG CCC TGC CGC AGG CAG AGC AAC CAC ACC TTC AGC AGC GGG GAC GTG		1526
Val Pro Cys Arg Arg Gln Ser Asn His Thr Phe Ser Ser Gly Asp Val		
435	440	445
GCC CCC TAC ACC AAG CTC TGC TGT AAG GGA TTC TGC ATC GAC ATC CTC		1574
Ala Pro Tyr Thr Lys Leu Cys Cys Lys Gly Phe Cys Ile Asp Ile Leu		
450	455	460

AAG AAG CTG GCC AGA GTG GTC AAA TTC TCC TAC GAC CTG TAC CTG GTG Lys Lys Leu Ala Arg Val Val Lys Phe Ser Tyr Asp Leu Tyr Leu Val 465 470 475	1622
ACT AAC GGC AAG CAT GGC AAG CGG GTG CCG GGC GTA TGG AAC GGC ATG Thr Asn Gly Lys His Gly Lys Arg Val Arg Gly Val Trp Asn Gly Met 480 485 490	1670
ATT GGG GAG GTG TAC TAC AAG CGG GCA GAC ATG GCC ATC GGC TCC CTC Ile Gly Glu Val Tyr Tyr Lys Arg Ala Asp Met Ala Ile Gly Ser Leu 495 500 505 510	1718
ACC ATC AAT GAG GAA CGC TCC GAG ATC GTA GAC TTC TCT GTA CCC TTT Thr Ile Asn Glu Glu Arg Ser Glu Ile Val Asp Phe Ser Val Pro Phe 515 520 525	1766
G TG GAG ACG GGC ATC AGT GTG ATG GTG GCT CGC AGC AAT GGC ACC GTC Val Glu Thr Gly Ile Ser Val Met Val Ala Arg Ser Asn Gly Thr Val 530 535 540	1814
TCC CCC TCG GCC TTC TTG GAG CCA TAT AGC CCT GCA GTG TGG GTG ATG Ser Pro Ser Ala Phe Leu Glu Pro Tyr Ser Pro Ala Val Trp Val Met 545 550 555	1862
ATG TTT GTC ATG TGC CTC ACT GTG GTG GCC ATC ACC GTC TTC ATG TTC Met Phe Val Met Cys Leu Thr Val Val Ala Ile Thr Val Phe Met Phe 560 565 570	1910
GAG TAC TTC AGC CCT GTC AGC TAC AAC CAG AAC CTC ACC AGA GGC AAG Glu Tyr Phe Ser Pro Val Ser Tyr Asn Gln Asn Leu Thr Arg Gly Lys 575 580 585 590	1958
AAG TCC GGG GGC CCA GCT TTI ACT ATC GGC AAG TCC GTG TGG CTG CTG Lys Ser Gly Gly Pro Ala Phe Thr Ile Gly Lys Ser Val Trp Leu Leu 595 600 605	2006
TGG GCG CTG GTC TTC AAC AAC TCA GTG CCC ATC GAG AAC CCG CGG GGC Trp Ala Leu Val Phe Asn Asn Ser Val Pro Ile Glu Asn Pro Arg Gly 610 615 620	2054
ACC ACC AGC AAG ATC ATG GTT CTG GTG TGG GCC TTC TTT GCT GTC ATC Thr Thr Ser Lys Ile Met Val Leu Val Trp Ala Phe Phe Ala Val Ile 625 630 635	2102
TTC CTC GCC AGA TAC ACG GCC AAC CTG GCC GCC TTC ATG ATC CAA GAG Phe Leu Ala Arg Tyr Thr Ala Asn Leu Ala Phe Met Ile Gln Glu 640 645 650	2150
CAA TAC ATC GAC ACT GTG TCG GGC CTC AGT GAC AAG AAG TTT CAG CGG Gln Tyr Ile Asp Thr Val Ser Gly Leu Ser Asp Lys Lys Phe Gln Arg 655 660 665 670	2198
CCT CAA GAT CAG TAC CCA CCT TTC CGC TTC GGC ACG GTG CCC AAC GGC Pro Gln Asp Gln Tyr Pro Pro Phe Arg Phe Gly Thr Val Pro Asn Gly 675 680 685	2246
AGC ACG GAG CGG AAC ATC CGC AGT AAC TAC CGT GAC ATG CAC ACC CAC Ser Thr Glu Arg Asn Ile Arg Ser Asn Tyr Arg Asp Met His Thr His 690 695 700	2294
ATG GTC AAG TTC AAC CAG CGC TCG GTG GAG GAC GCG CTC ACC AGC CTC Met Val Lys Phe Asn Gln Arg Ser Val Glu Asp Ala Leu Thr Ser Leu 705 710 715	2342
AAG ATG GGC TCT GAG GCT CAG CCT GTG CCC AGG AAG CTG GAT GCC TTC Lys Met Gly Ser Glu Ala Gln Pro Val Pro Arg Lys Leu Asp Ala Phe 720 725 730	2390

ATC TAT GAT GCT GCT GTC CTC AAC TAC ATG GCA GGC AAG GAC GAG GGC Ile Tyr Asp Ala Ala Val Leu Asn Tyr Met Ala Gly Lys Asp Glu Gly 735 740 745 750	2438
TGC AAG CTG GTC ACC ATT GGG TCT GGC AAG GTC TTT GCT ACC ACT GGC Cys Lys Leu Val Thr Ile Gly Ser Gly Lys Val Phe Ala Thr Thr Gly 755 760 765	2486
TAC GGC ATC GCC ATG CAG AAG GAC TCC CAC TGG AAG CGG GCC ATA GAC Tyr Gly Ile Ala Met Gln Lys Asp Ser His Trp Lys Arg Ala Ile Asp 770 775 780	2534
CTG GCG CTC TTG CAG TTC CTG GGG GAC GGA GAG ACA CAG AAA CTG GAG Leu Ala Leu Leu Gln Phe Leu Gly Asp Gly Glu Thr Gln Lys Leu Glu 785 790 795	2582
ACA GTG TGG CTC TCA GGG ATC TGC CAG AAT GAG AAG AAC GAG GTG ATG Thr Val Trp Leu Ser Gly Ile Cys Gln Asn Glu Lys Asn Glu Val Met 800 805 810	2630
AGC AGC AAG CTG GAC ATC GAC AAC ATG GGA GGC GTC TTC TAC ATG CTG Ser Ser Lys Leu Asp Ile Asp Asn Met Gly Gly Val Phe Tyr Met Leu 815 820 825 830	2678
CTG GTG GCC ATG GGG CTG GCC CTG CTG GTC TTC GCC TGG GAG CAC CTG Leu Val Ala Met Gly Leu Ala Leu Val Phe Ala Trp Glu His Leu 835 840 845	2726
GTC TAC TGG AAG CTG CGC CAC TCG GTG CCC AAC TCA TCC CAG CTG GAC Val Tyr Trp Lys Leu Arg His Ser Val Pro Asn Ser Ser Gln Leu Asp 850 855 860	2774
TTC CTG CTG GCT TTC AGC AGG GGC ATC TAC AGC TGC TTC AGC GGG GTG Phe Leu Leu Ala Phe Ser Arg Gly Ile Tyr Ser Cys Phe Ser Gly Val 865 870 875	2822
CAG AGC CTC GCC AGC CCA CCG CGG CAG GCC AGC CCG GAC CTC ACG GCC Gln Ser Leu Ala Ser Pro Pro Arg Gln Ala Ser Pro Asp Leu Thr Ala 880 885 890	2870
AGC TCG GCC CAG GCC AGC GTG CTC AAG ATT CTG CAG GCA GCC CGC GAC Ser Ser Ala Gln Ala Ser Val Leu Lys Ile Leu Gln Ala Ala Arg Asp 895 900 905 910	2918
ATG GTG ACC ACG GCG GGC GTA AGC AAC TCC CTG GAC CGC GCC ACT CGC Met Val Thr Ala Gly Val Ser Asn Ser Leu Asp Arg Ala Thr Arg 915 920 925	2966
ACC ATC GAG AAT TGG GGT GGC GGC CGC CGT GCG CCC CCA CCG TCC CCC Thr Ile Glu Asn Trp Gly Gly Arg Arg Ala Pro Pro Pro Ser Pro 930 935 940	3014
TGC CCG ACC CCG CGG TCT GGC CCC AGC CCA TGC CTG CCC ACC CCC GAC Cys Pro Thr Pro Arg Ser Gly Pro Ser Pro Cys Leu Pro Thr Pro Asp 945 950 955	3062
CCG CCC CCA GAG CCG AGC CCC ACG GGC TGG GGA CCG CCA GAC GGG GGT Pro Pro Pro Glu Pro Ser Pro Thr Gly Trp Gly Pro Pro Asp Gly Gly 960 965 970	3110
CGC GCG GCG CTT GTG CGC AGG GCT CCG CAG CCC CGG GGC CGC CCC CCG Arg Ala Ala Leu Val Arg Arg Ala Pro Gln Pro Pro Gly Arg Pro Pro 975 980 985 990	3158
ACG CCG GGG CCG CCC CTG TCC GAC GTC TCC CGA GTG TCG CGC CGC CCA Thr Pro Gly Pro Pro Leu Ser Asp Val Ser Arg Val Ser Arg Arg Pro 995 1000 1005	3206

GCC TGG GAG GCG CGG TGG CCG GTG CGG ACC GGG CAC TGC GGG AGG CAC Ala Trp Glu Ala Arg Trp Pro Val Arg Thr Gly His Cys Gly Arg His 1010 1015 1020	3254
CTC TCG GCC TCC GAG CGG CCC CTG TCG CCC GCG CGC TGT CAC TAC AGC Leu Ser Ala Ser Glu Arg Pro Leu Ser Pro Ala Arg Cys His Tyr Ser 1025 1030 1035	3302
TCC TTT CCT CGA GCC GAC CGA TCC GGC CGC CCC TTC CTC CCG CTC TTC Ser Phe Pro Arg Ala Asp Arg Ser Gly Arg Pro Phe Leu Pro Leu Phe 1040 1045 1050	3350
CCG GAG CCC CCG GAG CTG GAG GAC CTG CCG CTG CTC GGT CCG GAG CAG Pro Glu Pro Pro Glu Leu Glu Asp Leu Pro Leu Leu Gly Pro Glu Gln 1055 1060 1065 1070	3398
CTG GCC CGG CGG GAG GCC CTG CTG AAC GCG GCC TGG GCC CGG GGC TCG Leu Ala Arg Arg Glu Ala Leu Leu Asn Ala Ala Trp Ala Arg Gly Ser 1075 1080 1085	3446
CGC CCG AGT CAC GCT TCC CTG CCC AGC TCC GTG GCC GAG GCC TTC GCT Arg Pro Ser His Ala Ser Leu Pro Ser Ser Val Ala Glu Ala Phe Ala 1090 1095 1100	3494
CGG CCC AGC TCG CTG CCC GCT GGG TGC ACC GGC CCC GCC TGC GCC CGC Arg Pro Ser Ser Leu Pro Ala Gly Cys Thr Gly Pro Ala Cys Ala Arg 1105 1110 1115	3542
CCC GAC GGC CAC TCG GCC TGC AGG CGC TTG GCG CAG GCG CAG TCG ATG Pro Asp Gly His Ser Ala Cys Arg Arg Leu Ala Gln Ala Gln Ser Met 1120 1125 1130	3590
TGC TTG CCG ATC TAC CGG GAG GCC TGC CAG GAG GGC GAG CAG GCA GGG Cys Leu Pro Ile Tyr Arg Glu Ala Cys Gln Glu Gly Glu Gln Ala Gly 1135 1140 1145 1150	3638
GCC CCC GCC TGG CAG CAC AGA CAG CAC GTC TGC CTG CAC GCC CAC GCC Ala Pro Ala Trp Gln His Arg Gln His Val Cys Leu His Ala His Ala 1155 1160 1165	3686
CAC CTG CCA TTG TGC TGG GGG GCT GTC TGT CCT CAC CTT CCA CCC TGT His Leu Pro Leu Cys Trp Gly Ala Val Cys Pro His Leu Pro Pro Cys 1170 1175 1180	3734
GAC AGC CAC GGC TCC TGG CTC TCC GGC GCC TGG GGG CCT CTG GGG CAC Asp Ser His Gly Ser Trp Leu Ser Gly Ala Trp Gly Pro Leu Gly His 1185 1190 1195	3782
AGC GGC AGG ACT CTG GGG CTG GGC ACA GGC TAC AGA GAC AGT GGG GGA Ser Gly Arg Thr Leu Gly Leu Gly Thr Gly Tyr Arg Asp Ser Gly Gly 1200 1205 1210	3830
CTG GAC GAG ATC AGC AGT GTA GCC CGT GGG ACG CAA GGC TTC CCG GGA Leu Asp Glu Ile Ser Ser Val Ala Arg Gly Thr Gln Gly Phe Pro Gly 1215 1220 1225 1230	3878
CCC TGC ACC TGG AGA CGG ATC TCC AGT CTG GAG TCA GAA GTG TGAGTTATCA Pro Cys Thr Trp Arg Arg Ile Ser Ser Leu Glu Ser Glu Val 1235 1240 124	3930
GCCACTCAGG CTCCGAGCCA GCTGGATTCT CTGCCTGCCA CTGTCAGGGT TAAGCGGCAG	3990
GCAGGATTGG CCCTTCTCTG GCTTCTACCA TGAAATCCTG GCCATGGCAC CCCAGTGACA	4050
GATGATGTCT TCCATGGTCA TCAGTGACCT CAGCTAGCCT CA	4092

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1244 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

Met Gly Gly Ala Leu Gly Pro Ala Leu Leu Leu Thr Ser Leu Phe Gly
1 5 10 15

Ala Trp Ala Gly Leu Gly Pro Gly Gln Gly Glu Gln Gly Met Thr Val
20 25 30

Ala Val Val Phe Ser Ser Ser Gly Pro Pro Gln Ala Gln Phe Arg Val
35 40 45

Arg Leu Thr Pro Gln Ser Phe Leu Asp Leu Pro Leu Glu Ile Gln Pro
50 55 60

Leu Thr Val Gly Val Asn Thr Thr Asn Pro Ser Ser Leu Leu Thr Gln
65 70 75 80

Ile Cys Gly Leu Leu Gly Ala Ala His Val His Gly Ile Val Phe Glu
85 90 95

Asp Asn Val Asp Thr Glu Ala Val Ala Gln Ile Leu Asp Phe Ile Ser
100 105 110

Ser Gln Thr His Val Pro Ile Leu Ser Ile Ser Gly Gly Ser Ala Val
115 120 125

Val Leu Thr Pro Lys Glu Pro Gly Ser Ala Phe Leu Gln Leu Gly Val
130 135 140

Ser Leu Glu Gln Gln Leu Gln Val Leu Phe Lys Val Leu Glu Glu Tyr
145 150 155 160

Asp Trp Ser Ala Phe Ala Val Ile Thr Ser Leu His Pro Gly His Ala
165 170 175

Leu Phe Leu Glu Gly Val Arg Ala Val Ala Asp Ala Ser His Val Ser
180 185 190

Trp Arg Leu Leu Asp Val Val Thr Leu Glu Leu Asp Pro Gly Gly Pro
195 200 205

Arg Ala Arg Thr Gln Arg Leu Leu Arg Gln Leu Asp Ala Pro Val Phe
210 215 220

Val Ala Tyr Cys Ser Arg Glu Glu Ala Glu Val Leu Phe Ala Glu Ala
225 230 235 240

Ala Gln Ala Gly Leu Val Gly Pro Gly His Val Trp Leu Val Pro Asn
245 250 255

Leu Ala Leu Gly Ser Thr Asp Ala Pro Pro Ala Thr Phe Pro Val Gly
260 265 270

Leu Ile Ser Val Val Thr Glu Ser Trp Arg Leu Ser Leu Arg Gln Lys
275 280 285

Val Arg Asp Gly Val Ala Ile Leu Ala Leu Gly Ala His Ser Tyr Trp

290	295	300
Arg Gln His Gly Thr Leu Pro Ala Pro Ala Gly Asp Cys Arg Val His		
305	310	315
320		
Pro Gly Pro Val Ser Pro Ala Arg Glu Ala Phe Tyr Arg His Leu Leu		
325	330	335
Asn Val Thr Trp Glu Gly Arg Asp Phe Ser Phe Ser Pro Gly Gly Tyr		
340	345	350
Leu Val Gln Pro Thr Met Val Val Ile Ala Leu Asn Arg His Arg Leu		
355	360	365
Trp Glu Met Val Gly Arg Trp Glu His Gly Val Leu Tyr Met Lys Tyr		
370	375	380
Pro Val Trp Pro Arg Tyr Ser Ala Ser Leu Gln Pro Val Val Asp Ser		
385	390	395
400		
Arg His Leu Thr Val Ala Thr Leu Glu Glu Arg Pro Phe Val Ile Val		
405	410	415
Glu Ser Pro Asp Pro Gly Thr Gly Gly Cys Val Pro Asn Thr Val Pro		
420	425	430
Cys Arg Arg Gln Ser Asn His Thr Phe Ser Ser Gly Asp Val Ala Pro		
435	440	445
Tyr Thr Lys Leu Cys Cys Lys Gly Phe Cys Ile Asp Ile Leu Lys Lys		
450	455	460
Leu Ala Arg Val Val Lys Phe Ser Tyr Asp Leu Tyr Leu Val Thr Asn		
465	470	475
480		
Gly Lys His Gly Lys Arg Val Arg Gly Val Trp Asn Gly Met Ile Gly		
485	490	495
Glu Val Tyr Tyr Lys Arg Ala Asp Met Ala Ile Gly Ser Leu Thr Ile		
500	505	510
Asn Glu Glu Arg Ser Glu Ile Val Asp Phe Ser Val Pro Phe Val Glu		
515	520	525
Thr Gly Ile Ser Val Met Val Ala Arg Ser Asn Gly Thr Val Ser Pro		
530	535	540
Ser Ala Phe Leu Glu Pro Tyr Ser Pro Ala Val Trp Val Met Met Phe		
545	550	555
560		
Val Met Cys Leu Thr Val Val Ala Ile Thr Val Phe Met Phe Glu Tyr		
565	570	575
Phe Ser Pro Val Ser Tyr Asn Gln Asn Leu Thr Arg Gly Lys Lys Ser		
580	585	590
Gly Gly Pro Ala Phe Thr Ile Gly Lys Ser Val Trp Leu Leu Trp Ala		
595	600	605
Leu Val Phe Asn Asn Ser Val Pro Ile Glu Asn Pro Arg Gly Thr Thr		
610	615	620
Ser Lys Ile Met Val Leu Val Trp Ala Phe Phe Ala Val Ile Phe Leu		
625	630	635
640		
Ala Arg Tyr Thr Ala Asn Leu Ala Ala Phe Met Ile Gln Glu Gln Tyr		

645	650	655
Ile Asp Thr Val Ser Gly Leu Ser Asp Lys Lys Phe Gln Arg Pro Gln 660	665	670
Asp Gln Tyr Pro Pro Phe Arg Phe Gly Thr Val Pro Asn Gly Ser Thr 675	680	685
Glu Arg Asn Ile Arg Ser Asn Tyr Arg Asp Met His Thr His Met Val 690	695	700
Lys Phe Asn Gln Arg Ser Val Glu Asp Ala Leu Thr Ser Leu Lys Met 705	710	715
Gly Ser Glu Ala Gln Pro Val Pro Arg Lys Leu Asp Ala Phe Ile Tyr 725	730	735
Asp Ala Ala Val Leu Asn Tyr Met Ala Gly Lys Asp Glu Gly Cys Lys 740	745	750
Leu Val Thr Ile Gly Ser Gly Lys Val Phe Ala Thr Thr Gly Tyr Gly 755	760	765
Ile Ala Met Gln Lys Asp Ser His Trp Lys Arg Ala Ile Asp Leu Ala 770	775	780
Leu Leu Gln Phe Leu Gly Asp Gly Glu Thr Gln Lys Leu Glu Thr Val 785	790	795
Trp Leu Ser Gly Ile Cys Gln Asn Glu Lys Asn Glu Val Met Ser Ser 805	810	815
Lys Leu Asp Ile Asp Asn Met Gly Gly Val Phe Tyr Met Leu Leu Val 820	825	830
Ala Met Gly Leu Ala Leu Leu Val Phe Ala Trp Glu His Leu Val Tyr 835	840	845
Trp Lys Leu Arg His Ser Val Pro Asn Ser Ser Gln Leu Asp Phe Leu 850	855	860
Leu Ala Phe Ser Arg Gly Ile Tyr Ser Cys Phe Ser Gly Val Gln Ser 865	870	875
Leu Ala Ser Pro Pro Arg Gln Ala Ser Pro Asp Leu Thr Ala Ser Ser 885	890	895
Ala Gln Ala Ser Val Leu Lys Ile Leu Gln Ala Ala Arg Asp Met Val 900	905	910
Thr Thr Ala Gly Val Ser Asn Ser Leu Asp Arg Ala Thr Arg Thr Ile 915	920	925
Glu Asn Trp Gly Gly Arg Arg Ala Pro Pro Pro Ser Pro Cys Pro 930	935	940
Thr Pro Arg Ser Gly Pro Ser Pro Cys Leu Pro Thr Pro Asp Pro Pro 945	950	955
Pro Glu Pro Ser Pro Thr Gly Trp Gly Pro Pro Asp Gly Gly Arg Ala 965	970	975
Ala Leu Val Arg Arg Ala Pro Gln Pro Pro Gly Arg Pro Pro Thr Pro 980	985	990
Gly Pro Pro Leu Ser Asp Val Ser Arg Val Ser Arg Arg Pro Ala Trp		

995	1000	1005
Glu Ala Arg Trp Pro Val Arg Thr Gly His Cys Gly Arg His Leu Ser		
1010	1015	1020
Ala Ser Glu Arg Pro Leu Ser Pro Ala Arg Cys His Tyr Ser Ser Phe		
1025	1030	1035
1040		
Pro Arg Ala Asp Arg Ser G	Arg Pro Phe Leu Pro Leu Phe Pro Glu	
1045	1050	1055
Pro Pro Glu Leu Glu Asp Leu Pro Leu Leu Gly Pro Glu Gln Leu Ala		
1060	1065	1070
Arg Arg Glu Ala Leu Leu Asn Ala Ala Trp Ala Arg Gly Ser Arg Pro		
1075	1080	1085
Ser His Ala Ser Leu Pro Ser Ser Val Ala Glu Ala Phe Ala Arg Pro		
1090	1095	1100
Ser Ser Leu Pro Ala Gly Cys Thr Gly Pro Ala Cys Ala Arg Pro Asp		
1105	1110	1115
1120		
Gly His Ser Ala Cys Arg Arg Leu Ala Gln Ala Gln Ser Met Cys Leu		
1125	1130	1135
Pro Ile Tyr Arg Glu Ala Cys Gln Glu Gly Glu Gln Ala Gly Ala Pro		
1140	1145	1150
Ala Trp Gln His Arg Gln His Val Cys Leu His Ala His Ala His Leu		
1155	1160	1165
Pro Leu Cys Trp Gly Ala Val Cys Pro His Leu Pro Pro Cys Asp Ser		
1170	1175	1180
His Gly Ser Trp Leu Ser Gly Ala Trp Gly Pro Leu Gly His Ser Gly		
1185	1190	1195
1200		
Arg Thr Leu Gly Leu Gly Thr Gly Tyr Arg Asp Ser Gly Gly Leu Asp		
1205	1210	1215
Glu Ile Ser Ser Val Ala Arg Gly Thr Gln Gly Phe Pro Gly Pro Cys		
1220	1225	1230
Thr Trp Arg Arg Ile Ser Ser Leu Glu Ser Glu Val		
1235	1240	

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4053 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 189..3884

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

CCCTTAATAAA GATTTGCNAC GTACACTCGA GCCATGGCGA GTGTCTTGA CCCGCGGGTG	60
ACGGTGGCTC TCGCTGCTCG CGCCCCCTCC TCCCAGGGGG GGAGCCTGAT GCCACGTTCC	120
CTATGAATTA TTTATCGCCG GCCTAAAAAT ACCCGAAGT TCACAGCCCC AGTGACCCCTC	180
CGGTGGAC ATG GGT GGG GCC CTG GGG CCG GCC CTG TTG CTC ACC TCG CTC Met Gly Ala Leu Gly Pro Ala Leu Leu Thr Ser Leu	230
1 5 10	
TTC GGT GCC TGG GCA GGG CTG GGT CCG GGG CAG GGC GAG CAG GGC ATG Phe Gly Ala Trp Ala Gly Leu Gly Pro Gly Gln Gly Glu Gln Gly Met	278
15 20 25 30	
ACG GTG GCC GTG GTG TTT AGC AGC TCA GGG CCG CCC CAG GCC CAG TTC Thr Val Ala Val Val Phe Ser Ser Gly Pro Pro Gln Ala Gln Phe	326
35 40 45	
CGT GTC CGC CTC ACC CCC CAG AGC TTC CTG GAC CTA CCC CTG GAG ATC Arg Val Arg Leu Thr Pro Gln Ser Phe Leu Asp Leu Pro Leu Glu Ile	374
50 55 60	
CAG CCG CTC ACA GTT GGG GTC AAC ACC ACC AAC CCC AGC AGC CTC CTC Gln Pro Leu Thr Val Gly Val Asn Thr Thr Asn Pro Ser Ser Leu Leu	422
65 70 75	
ACC CAG ATC TGC GGC CTC CTG GGT GCT GCC CAC GTC CAC GGC ATT GTC Thr Gln Ile Cys Gly Leu Leu Gly Ala Ala His Val His Gly Ile Val	470
80 85 90	
TTT GAG GAC AAC GTG GAC ACC GAG GCG GTG GCC CAG ATC CTT GAC TTC Phe Glu Asp Asn Val Asp Thr Glu Ala Val Ala Gln Ile Leu Asp Phe	518
95 100 105 110	
ATC TCC TCC CAG ACC CAT GTG CCC ATC CTC AGC ATC AGC GGA GGC TCT Ile Ser Ser Gln Thr His Val Pro Ile Leu Ser Ile Ser Gly Gly Ser	566
115 120 125	
GCT GTG GTC CTC ACC CCC AAG GAG CCG GGC TCC GCC TTC CTG CAG CTG Ala Val Val Leu Thr Pro Lys Glu Pro Gly Ser Ala Phe Leu Gln Leu	614
130 135 140	
GGC GTG TCC CTG GAG CAG CAG CTG CAG GTG CTG TTC AAG GTG CTG GAA Gly Val Ser Leu Glu Gln Gln Val Leu Phe Lys Val Leu Glu	662
145 150 155	
GAG TAC GAC TGG AGC GCC TTC GCC GTC ATC ACC AGC CTG CAC CCG GGC Glu Tyr Asp Trp Ser Ala Phe Ala Val Ile Thr Ser Leu His Pro Gly	710
160 165 170	
CAC GCG CTC TTC CTG GAG GGC GTG CGC GCC GTC GCC GAC GCC AGC CAC His Ala Leu Phe Leu Glu Gly Val Arg Ala Val Ala Asp Ala Ser His	758
175 180 185 190	
GTG AGT TGG CGG CTG CTG GAC GTG GTC ACG CTG GAA CTG GAC CCG GGA Val Ser Trp Arg Leu Leu Asp Val Val Thr Leu Glu Leu Asp Pro Gly	806
195 200 205	
GGG CGG CGC GCG CGC ACG CAG CGC CTG CTG CGC TAG CTC GAC GCG CCC Gly Pro Arg Ala Arg Thr Gln Arg Leu Leu Arg Gln Leu Asp Ala Pro	854
210 215 220	
GTG TTT GTG GCC TAC TGC TCG CGC GAG GAG GCC GAG GTG CTC TTC GCC Val Phe Val Ala Tyr Cys Ser Arg Glu Glu Ala Glu Val Leu Phe Ala	902
225 230 235	

GAG	GCG	GCG	CAG	GCC	GGT	CTG	GTG	GGP	CCC	GGC	CAC	GTG	TGG	CTG	GTG		950
Glu	Ala	Ala	Gln	Ala	Gly	Leu	Val	Gly	Phe	Gly	His	Val	Trp	Leu	Val		
240					245						250						
CCC	AAC	CTG	GCG	CTG	GGC	AGC	ACC	GAT	GCG	CCC	CCC	GCC	ACC	TTC	CCC		998
Pro	Asn	Leu	Ala	Leu	Gly	Ser	Thr	Asp	Aia	Pro	Pro	Ala	Thr	Phe	Pro		
255					260					265					270		
GTG	GGC	CTC	ATC	AGC	GTC	GTC	ACC	GAG	AGC	TGG	CGC	CTC	AGC	CTG	CGC		1046
Val	Gly	Leu	Ile	Ser	Val	Val	Thr	Glu	Ser	Trp	Arg	Leu	Ser	Leu	Arg		
275							280					285					
CAG	AAG	GTG	CGC	GAC	GGC	GTG	GCC	ATT	CTG	GCC	CTG	GGC	GCC	CAC	AGC		1094
Gln	Lys	Val	Arg	Asp	Gly	Val	Ala	Ile	Leu	Ala	Leu	Gly	Ala	His	Ser		
290							295					300					
TAC	TGG	CGC	CAG	CAT	GGA	ACC	CTG	CCA	GCC	CCG	GCC	GGG	GAC	TGC	CGT		1142
Tyr	Trp	Arg	Gln	His	Gly	Thr	Leu	Pro	Ala	Pro	Ala	Gly	Asp	Cys	Arg		
305							310					315					
GTT	CAC	CCT	GGG	CCC	GTC	AGC	CCT	GCC	CGG	GAG	GCC	TTC	TAC	AGG	CAC		1190
Val	His	Pro	Gly	Pro	Val	Ser	Pro	Ala	Arg	Glu	Ala	Phe	Tyr	Arg	His		
320						325				330							
CTA	CTG	AAT	GTC	ACC	TGG	GAG	GGC	CGA	GAC	TTC	TCC	TTC	AGC	CCT	GGT		1238
Leu	Leu	Asn	Val	Thr	Trp	Glu	Gly	Arg	Asp	Phe	Ser	Phe	Ser	Pro	Gly		
335						340				345					350		
GGG	TAC	CTG	GTC	CAG	CCC	ACC	ATG	GTG	GTG	ATC	GCC	CTC	AAC	CGG	CAC		1286
Gly	Tyr	Leu	Val	Gln	Pro	Thr	Met	Val	Val	Ile	Ala	Leu	Asn	Arg	His		
355								360					365				
CGC	CTC	TGG	GAG	ATG	GTG	GGG	CGC	TGG	GAG	CAT	GGC	GTC	CTA	TAC	ATG		1334
Arg	Leu	Trp	Glu	Met	Val	Gly	Arg	Trp	Glu	His	Gly	Val	Leu	Tyr	Met		
370							375					380					
AAG	TAC	CCC	GTG	TGG	CCT	CGC	TAC	AGT	GCC	TCT	CTG	CAG	CCT	GTG	GTG		1382
Lys	Tyr	Pro	Val	Trp	Pro	Arg	Tyr	Ser	Ala	Ser	Leu	Gln	Pro	Val	Val		
385							390					395					
GAC	AGT	CGG	CAC	CTG	ACG	GTG	GCT	ACG	CTG	GAA	GAG	CGG	CCC	TTT	GTC		1430
Asp	Ser	Arg	His	Leu	Thr	Val	Ala	Thr	Leu	Glu	Glu	Arg	Pro	Phe	Val		
400							405				410						
ATC	GTG	GAG	AGC	CCT	GAC	CCT	GGC	ACA	GGA	GGC	TGT	GTC	CCC	AAC	ACC		1478
Ile	Val	Glu	Ser	Pro	Asp	Pro	Gly	Thr	Gly	Gly	Cys	Val	Pro	Asn	Thr		
415						420				425				430			
GTG	CCC	TGC	CGC	AGG	CAG	AGC	AAC	CAC	ACC	TTC	AGC	AGT	GGG	GAC	GTG		1526
Val	Pro	Cys	Arg	Arg	Gln	Ser	Asn	His	Thr	Phe	Ser	Ser	Gly	Asp	Val		
435								440					445				
GCC	CCC	TAC	ACC	AAG	CTC	TGC	TGT	AAG	GGA	TTC	TGC	ATC	GAC	ATC	CTC		1574
Ala	Pro	Tyr	Thr	Lys	Leu	Cys	Cys	Lys	Gly	Phe	Cys	Ile	Asp	Ile	Leu		
450							455					460					
AAG	AAG	CTG	GCC	AGA	GTG	GTC	AAA	TTC	TCC	TAC	GAC	CTG	TAC	CTG	GTG		1622
Lys	Lys	Leu	Ala	Arg	Val	Val	Lys	Phe	Ser	Tyr	Asp	Leu	Tyr	Leu	Val		
465							470					475					
ACC	AAC	GGC	AAG	CAT	GGC	AAG	CGG	GTG	CGC	GGC	GTA	TGG	AAC	GGC	ATG		1670
Thr	Asn	Gly	Lys	His	Gly	Lys	Arg	Val	Arg	Gly	Val	Trp	Asn	Gly	Met		
480							485					490					
ATT	GGG	GA3	GTG	TAC	TAC	AAG	CGG	GCA	GAC	ATG	GCC	ATC	GGC	TCC	CTC		1718
Ile	Gly	Glu	Val	Tyr	Tyr	Lys	Arg	Ala	Asp	Met	Ala	Ile	Gly	Ser	Leu		
495							500					505			510		

ACC ATC AAT GAG GAA CGC TCC GAG ATC GTA GAC TTC TCT GTA CCC TTT Thr Ile Asn Glu Glu Arg Ser Glu Ile Val Asp Phe Ser Val Pro Phe 515 520 525	1766
GTG GAG ACG GGC ATC AGT GTG ATG GTG GCT CGC AG_ AAT GGC ACC GTC Val Glu Thr Gly Ile Ser Val Met Val Ala Arg Ser Asn Gly Thr Val 530 535 540	1814
TCC CCC TCG GCC TTC TTG GAG CCA TAT AGC CCT GCA GTG TGG GTG ATG Ser Pro Ser Ala Phe Leu Glu Pro Tyr Ser Pro Ala Val Trp Val Met 545 550 555	1862
ATG TTT GTC ATG TGC CTC ACT GTG GTG GCC ATC ACC GTC TTC ATG TTC Met Phe Val Met Cys Leu Thr Val Val Ala Ile Thr Val Phe Met Phe 560 565 570	1910
GAG TAC TTC AGC CCT GTC AGC TAC AAC CAG AAC CTC ACC AGA GGC AAG Glu Tyr Phe Ser Pro Val Ser Tyr Asn Gln Asn Leu Thr Arg Gly Lys 575 580 585 590	1958
ACT TTC ACT ATC GGC AAG TCC GTG TGG CTG CTG TGG GCG CTG GTC TTC Thr Phe Thr Ile Gly Lys Ser Val Trp Leu Leu Trp Ala Leu Val Phe 595 600 605	2006
AAC AAC TCA GTG CCC ATC GAG AAC CCG CGG GGC ACC ACC AGC AAG ATC Asn Asn Ser Val Pro Ile Glu Asn Pro Arg Gly Thr Thr Ser Lys Ile 610 615 620	2054
ATG GTT CTG GTC TGG GCC TTC TTT GCT GTC ATC TTC CTC GCC AGA TAC Met Val Leu Val Trp Ala Phe Ala Val Ile Phe Leu Ala Arg Tyr 625 630 635	2102
ACG GCC AAC CTG GCC GCC TTC ATG ATC CAA GAG CAA TAC ATC GAC ACT Thr Ala Asn Leu Ala Phe Met Ile Gln Glu Gln Tyr Ile Asp Thr 640 645 650	2150
GTG TCG GGC CTC AGT GAC AAG AAG TTT CAG CGG CCT CAA GAT CAG TAC Val Ser Gly Leu Ser Asp Lys Lys Phe Gln Arg Pro Gln Asp Gln Tyr 655 660 665 670	2198
CCA CCT TTC CGC TTC GGC ACG GTG CCC AAC GGC AGC ACG GAG CGG AAC Pro Pro Phe Arg Phe Gly Thr Val Pro Asn Gly Ser Thr Glu Arg Asn 675 680 685	2246
ATC CGC AGT AAC TAC CGT GAC ATG CAC ACC CAC ATG GTC AAG TTC AAC Ile Arg Ser Asn Tyr Arg Asp Met His Thr His Met Val Lys Phe Asn 690 695 700	2294
CAG CGC TCG GTG GAG GAC GCG CTC ACC AGC CTC AAG ATG GGG AAG CTG Gln Arg Ser Val Glu Asp Ala Leu Thr Ser Leu Lys Met Gly Lys Leu 705 710 715	2342
GAT GCT TTC ATC TAT GAT GCT GCT GTC CTC AAC TAC ATG GCA GGC AAG Asp Ala Phe Ile Tyr Asp Ala Ala Val Leu Asn Tyr Met Ala Gly Lys 720 725 730	2390
GAC GAG GGC TGC AAG CTG GTC ACC ATT GGG TCT GGC AAG GTC TTT GCT Asp Glu Gly Cys Lys Leu Val Thr Ile Gly Ser Gly Lys Val Phe Ala 735 740 745 750	2438
ACC ACT GGC TAC GGC ATC GCC ATG CAG AAG GAC TCC CAC TGG AAG CGG Thr Thr Gly Tyr Gly Ile Ala Met Gln Lys Asp Ser His Trp Lys Arg 755 760 765	2486
GCC ATA GAC CTG GCG CTC TTG CAG TTC CTG GGG GAC GGA GAG ACA CAG Ala Ile Asp Leu Ala Leu Leu Gln Phe Leu Gly Asp Gly Glu Thr Gln 770 775 780	2534

AAA CTG GAS ACA GTG TGG CTC TCA GGG ATC TGC CAG AAT GAG AAG AAC	2581
Lys Leu Glu Thr Val Trp Leu Ser Gly Ile Cys Gln Asn Glu Lys Asn	
785 790 795	
GAG GTG ATG AGC AGC AAG CTG GAC ATC GAC AAC ATG GGA GGC GTC TTC	2630
Glu Val Met Ser Ser Lys Leu Asp Ile Asp Asn Met Gly Gly Val Phe	
800 805 810	
TAC ATG CTG CTG GTG GCC ATG GGG CTG GCC CTG CTG GTC TTC GCC TGG	2678
Tyr Met Leu Leu Val Ala Met Gly Leu Ala Leu Leu Val Phe Ala Trp	
815 820 825 830	
GAG CAC CTG GTC TAC TGG AAG CTG CGC CAC TCG GTG CCC AAC TCA TCC	2726
Glu His Leu Val Tyr Trp Lys Leu Arg His Ser Val Pro Asn Ser Ser	
835 840 845	
CAG CTG GAC TTC CTG CTG GCT TTC AGC AGG GGC ATC TAC AGC TGC TTC	2774
Gln Leu Asp Phe Leu Leu Ala Phe Ser Arg Gly Ile Tyr Ser Cys Phe	
850 855 860	
AGC GGG GTG CAG AGC CTC GCC AGC CCA CCG CGG CAG GCC AGC CCG GAC	2822
Ser Gly Val Gln Ser Leu Ala Ser Pro Pro Arg Gln Ala Ser Pro Asp	
865 870 875	
CTC ACG GCC AGC TCG GCC CAG GCG AGC GTG CTC AAG ATT CTG CAG GCA	2870
Leu Thr Ala Ser Ser Ala Gln Ala Ser Val Leu Lys Ile Leu Gln Ala	
880 885 890	
GCC CGC GAC ATG GTG ACC ACG GCG GGC GTA AGC AAC TCC CTG GAC CGC	2918
Ala Arg Asp Met Val Thr Thr Ala Gly Val Ser Asn Ser Leu Asp Arg	
895 900 905 910	
GCC ACT CGC ACC ATC GAG AAT TGG GGT GGC GGC CGC CGT GCG CCC CCA	2966
Ala Thr Arg Thr Ile Glu Asn Trp Gly Gly Arg Arg Ala Pro Pro	
915 920 925	
CCG TCC CCC TGC CCG ACC CCG CGG TCT GGC CCC AGC CCA TGC CTG CCC	3014
Pro Ser Pro Cys Pro Thr Pro Arg Ser Gly Pro Ser Pro Cys Leu Pro	
930 935 940	
ACC CCC GAC CCG CCC CCA GAG CCG AGC CCC ACG GGC TGG GGA CCG CCA	3062
Thr Pro Asp Pro Pro Pro Glu Pro Ser Pro Thr Gly Trp Gly Pro Pro	
945 950 955	
GAC GGG GGT CGC GCG GCG CTT GTG CGC AGG GCT CCG CAG CCC CCG GGC	3110
Asp Gly Gly Arg Ala Ala Leu Val Arg Arg Ala Pro Gln Pro Pro Gly	
960 965 970	
CGC CCC CCG ACG CCG GGG CCG CCC CTG TCC GAC GTC TCC CGA GTG TCG	3158
Arg Pro Pro Thr Pro Gly Pro Pro Leu Ser Asp Val Ser Arg Val Ser	
975 980 985 990	
CGC CGC CCA GCC TGG GAG GCG CGG TGG CCG GTG CGG ACC GGG CAC TGC	3206
Arg Arg Pro Ala Trp Glu Ala Arg Trp Pro Val Arg Thr Gly His Cys	
995 1000 1005	
GGG AGG CAC CTC TCG GCC TCC GAG CGG CCC CTG TCG CCC GCG CGC TGT	3254
Gly Arg His Leu Ser Ala Ser Glu Arg Pro Leu Ser Pro Ala Arg Cys	
1010 1015 1020	
CAC TAC AGC TCC TTT CCT CGA GCG GAC CGA TCC GGC CGC CCC TTC TTC	3302
His Tyr Ser Ser Phe Pro Arg Ala Asp Arg Ser Gly Arg Pro Phe Leu	
1025 1030 1035	
CCG CTC TTC CCG GAG CCC CCG GAG CTG GAG GAC CTG CCG CTG CTC GGT	3350
Pro Leu Phe Pro Glu Pro Pro Glu Leu Glu Asp Leu Pro Leu Leu Gly	
1040 1045 1050	

CCG GAG CAG CTG GCC CGG CGG GAG GCC CTG CTG AAC GCG GCC TGG GCC Pro Glu Gln Leu Ala Arg Arg Glu Ala Leu Leu Asn Ala Ala Trp Ala 1055 1060 1065 1070	3398
CGG GGC TCG CGC CCG AGT CAC GCT TCC CTG CCC AGC TCC GTG GCC GAG Arg Gly Ser Arg Pro Ser His Ala Ser Leu Pro Ser Ser Val Ala Glu 1075 1080 1085	3446
GCC TTC GCT CGG CCC AGC TCG CTG CCC GCT GGG TGC ACC GGC CCC GCC Ala Phe Ala Arg Pro Ser Ser Leu Pro Ala Gly Cys Thr Gly Pro Ala 1090 1095 1100	3494
TGC GCC CGC CCC GAC GGC CAC TCG GCC TGC AGG CGC TTG GCG CAG GCG Cys Ala Arg Pro Asp Gly His Ser Ala Cys Arg Arg Leu Ala Gln Ala 1105 1110 1115	3542
CAG TCG ATG TGC TTG CCG ATC TAC CGG GAG GCC TGC CAG GAG GGC GAG Gln Ser Met Cys Leu Pro Ile Tyr Arg Glu Ala Cys Gln Glu Gly Glu 1120 1125 1130	3590
CAG GCA GGG GCC CCC GCC TGG CAG CAC AGA CAG CAC GTC TGC CTG CAC Gln Ala Gly Ala Pro Ala Trp Gln His Arg Gln His Val Cys Leu His 1135 1140 1145 1150	3638
GCC CAC GCC CAC CTG CCA TTG TGC TGG GGG GCT GTC TGT CCT CAC CTT Ala His Ala His Leu Pro Leu Cys Trp Gly Ala Val Cys Pro His Leu 1155 1160 1165	3686
CCA CCC TGT GAC AGC CAC GGC TCC TGG CTC TCC GGC GCC TGG GGG CCT Pro Pro Cys Asp Ser His Gly Ser Trp Leu Ser Gly Ala Trp Gly Pro 1170 1175 1180	3734
CTG GGG CAC AGC GGC AGG ACT CTG GGG CTG GGC ACA GGC TAC AGA GAC Leu Gly His Ser Gly Arg Thr Leu Gly Leu Gly Thr Gly Tyr Arg Asp 1185 1190 1195	3782
AGT GGG GGA CTG GAC GAG ATC AGC AGT GTA GCC CGT GGG ACG CAA GGC Ser Gly Gly Leu Asp Glu Ile Ser Ser Val Ala Arg Gly Thr Gln Gly 1200 1205 1210	3830
TTC CCG GGA CCC TGC ACC TGG AGA CGG ATC TCC AGT CTG GAG TCA GAA Phe Pro Gly Pro Cys Thr Trp Arg Arg Ile Ser Ser Leu Glu Ser Glu 1215 1220 1225 1230	3878
GTG TGAGTTATCA GCCACTCAGG CTCCGAGCCA GCTGGATTCT CTGCCTGCCA Val	3931
CTGTCAAGGT TAAGCGGCAG GCAGGATTGG CCTTCTCTG GCTTCTACCA TGAAATCCTG	3991
GCCATGGCAC CCCAGTGACA GATGATGTCT TCCATGGTCA TCAGTGACCT CAGCTAGCCT	4051
CA	4053

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1231 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

Met Gly Gly Ala Leu Gly Pro Ala Leu Leu Leu Thr Ser Leu Phe Gly

1	5	10	15
Ala Trp Ala Gly Leu Gly Pro Gly Gln Gly Glu Gln Gly Met Thr Val			
20	25	30	
Ala Val Val Phe Ser Ser Ser Gly Pro Pro Gln Ala Gln Phe Arg Val			
35	40	45	
Arg Leu Thr Pro Gln Ser Phe Leu Asp Leu Pro Leu Glu Ile Gln Pro			
50	55	60	
Leu Thr Val Gly Val Asn Thr Thr Asn Pro Ser Ser Leu Leu Thr Gln			
65	70	75	80
Ile Cys Gly Leu Leu Gly Ala Ala His Val His Gly Ile Val Phe Glu			
85	90	95	
Asp Asn Val Asp Thr Glu Ala Val Ala Gln Ile Leu Asp Phe Ile Ser			
100	105	110	
Ser Gln Thr His Val Pro Ile Leu Ser Ile Ser Gly Gly Ser Ala Val			
115	120	125	
Val Leu Thr Pro Lys Glu Pro Gly Ser Ala Phe Leu Gln Leu Gly Val			
130	135	140	
Ser Leu Glu Gln Gln Leu Gln Val Leu Phe Lys Val Leu Glu Glu Tyr			
145	150	155	160
Asp Trp Ser Ala Phe Ala Val Ile Thr Ser Leu His Pro Gly His Ala			
165	170	175	
Leu Phe Leu Glu Gly Val Arg Ala Val Ala Asp Ala Ser His Val Ser			
180	185	190	
Trp Arg Leu Leu Asp Val Val Thr Leu Glu Leu Asp Pro Gly Gly Pro			
195	200	205	
Arg Ala Arg Thr Gln Arg Leu Leu Arg Gln Leu Asp Ala Pro Val Phe			
210	215	220	
Val Ala Tyr Cys Ser Arg Glu Glu Ala Glu Val Leu Phe Ala Glu Ala			
225	230	235	240
Ala Gln Ala Gly Leu Val Gly Pro Gly His Val Trp Leu Val Pro Asn			
245	250	255	
Leu Ala Leu Gly Ser Thr Asp Ala Pro Pro Ala Thr Phe Pro Val Gly			
260	265	270	
Leu Ile Ser Val Val Thr Glu Ser Trp Arg Leu Ser Leu Arg Gln Lys			
275	280	285	
Val Arg Asp Gly Val Ala Ile Leu Ala Leu Gly Ala His Ser Tyr Trp			
290	295	300	
Arg Gln His Gly Thr Leu Pro Ala Pro Ala Gly Asp Cys Arg Val His			
305	310	315	320
Pro Gly Pro Val Ser Pro Ala Arg Glu Ala Phe Tyr Arg His Leu Leu			
325	330	335	
Asn Val Thr Trp Glu Gly Arg Asp Phe Ser Phe Ser Pro Gly Gly Tyr			
340	345	350	
Leu Val Gln Pro Thr Met Val Val Ile Ala Leu Asn Arg His Arg Leu			

355	360	365
Trp Glu Met Val Gly Arg Trp Glu His Gly Val Leu Tyr Met Lys Tyr 370	375	380
Pro Val Trp Pro Arg Tyr Ser Ala Ser Leu Gln Pro Val Val Asp Ser 385	390	395
Arg His Leu Thr Val Ala Thr Leu Glu Arg Pro Phe Val Ile Val 405	410	415
Glu Ser Pro Asp Pro Gly Thr Gly Cys Val Pro Asn Thr Val Pro 420	425	430
Cys Arg Arg Gln Ser Asn His Thr Phe Ser Ser Gly Asp Val Ala Pro 435	440	445
Tyr Thr Lys Leu Cys Cys Lys Gly Phe Cys Ile Asp Ile Leu Lys Lys 450	455	460
Leu Ala Arg Val Val Lys Phe Ser Tyr Asp Leu Tyr Leu Val Thr Asn 465	470	475
Gly Lys His Gly Lys Arg Val Arg Gly Val Trp Asn Gly Met Ile Gly 485	490	495
Glu Val Tyr Tyr Lys Arg Ala Asp Met Ala Ile Gly Ser Leu Thr Ile 500	505	510
Asn Glu Glu Arg Ser Glu Ile Val Asp Phe Ser Val Pro Phe Val Glu 515	520	525
Thr Gly Ile Ser Val Met Val Ala Arg Ser Asn Gly Thr Val Ser Pro 530	535	540
Ser Ala Phe Leu Glu Pro Tyr Ser Pro Ala Val Trp Val Met Met Phe 545	550	555
Val Met Cys Leu Thr Val Val Ala Ile Thr Val Phe Met Phe Glu Tyr 565	570	575
Phe Ser Pro Val Ser Tyr Asn Gln Asn Leu Thr Arg Gly Lys Thr Phe 580	585	590
Thr Ile Gly Lys Ser Val Trp Leu Leu Trp Ala Leu Val Phe Asn Asn 595	600	605
Ser Val Pro Ile Glu Asn Pro Arg Gly Thr Thr Ser Lys Ile Met Val 610	615	620
Leu Val Trp Ala Phe Phe Ala Val Ile Phe Leu Ala Arg Tyr Thr Ala 625	630	635
Asn Leu Ala Ala Phe Met Ile Gln Glu Gln Tyr Ile Asp Thr Val Ser 645	650	655
Gly Leu Ser Asp Lys Lys Phe Gln Arg Pro Gln Asp Gln Tyr Pro Pro 660	665	670
Phe Arg Phe Gly Thr Val Pro Asn Gly Ser Thr Glu Arg Asn Ile Arg 675	680	685
Ser Asn Tyr Arg Asp Met His Thr His Met Val Lys Phe Asn Gln Arg 690	695	700
Ser Val Glu Asp Ala Leu Thr Ser Leu Lys Met Gly Lys Leu Asp Ala		

705 710 715 720
Phe Ile Tyr Asp Ala Ala Val Leu Asn Tyr Met Ala Gly Lys Asp Glu
725 730 735
Gly Cys Lys Leu Val Thr Ile Gly Ser Gly Lys Val Phe Ala Thr Thr
740 745 750
Gly Tyr Gly Ile Ala Met Gln Lys Asp Ser His Trp Lys Arg Ala Ile
755 760 765
Asp Leu Ala Leu Leu Gln Phe Leu Gly Asp Gly Glu Thr Gln Lys Leu
770 775 780
Glu Thr Val Trp Leu Ser Gly Ile Cys Gln Asn Glu Lys Asn Glu Val
785 790 795 800
Met Ser Ser Lys Leu Asp Ile Asp Asn Met Gly Gly Val Phe Tyr Met
805 810 815
Leu Leu Val Ala Met Gly Leu Ala Leu Leu Val Phe Ala Trp Glu His
820 825 830
Leu Val Tyr Trp Lys Leu Arg His Ser Val Pro Asn Ser Ser Gln Leu
835 840 845
Asp Phe Leu Leu Ala Phe Ser Arg Gly Ile Tyr Ser Cys Phe Ser Gly
850 855 860
Val Gln Ser Leu Ala Ser Pro Pro Arg Gln Ala Ser Pro Asp Leu Thr
865 870 875 880
Ala Ser Ser Ala Gln Ala Ser Val Leu Lys Ile Leu Gln Ala Ala Arg
885 890 895

Asp Met Val Thr Thr Ala Gly Val Ser Asn Ser Leu Asp Arg Ala Thr
900 905 910
Arg Thr Ile Glu Asn Trp Gly Gly Arg Arg Ala Pro Pro Pro Ser
915 920 925
Pro Cys Pro Thr Pro Arg Ser Gly Pro Ser Pro Cys Leu Pro Thr Pro
930 935 940
Asp Pro Pro Pro Glu Pro Ser Pro Thr Gly Trp Gly Pro Pro Asp Gly
945 950 955 960
Gly Arg Ala Ala Leu Val Arg Arg Ala Pro Gln Pro Pro Gly Arg Pro
965 970 975
Pro Thr Pro Gly Pro Pro Leu Ser Asp Val Ser Arg Val Ser Arg Arg
980 985 990
Pro Ala Trp Glu Ala Arg Trp Pro Val Arg Thr Gly His Cys Gly Arg
995 1000 1005
His Leu Ser Ala Ser Glu Arg Pro Leu Ser Pro Ala Arg Cys His Tyr
1010 1015 1020
Ser Ser Phe Pro Arg Ala Asp Arg Ser Gly Arg Pro Phe Leu Pro Leu
1025 1030 1035 1040
Phe Pro Glu Pro Pro Glu Leu Glu Asp Leu Pro Leu Leu Gly Pro Glu
1045 1050 1055
Gln Leu Ala Arg Arg Glu Ala Leu Leu Asn Ala Ala Trp Ala Arg Gly

1060	1065	1070
Ser Arg Pro Ser His Ala Ser Leu Pro Ser Ser Val Ala Glu Ala Phe		
1075	1080	1085
Ala Arg Pro Ser Ser Leu Pro Ala Gly Cys Thr Gly Pro Ala Cys Ala		
1090	1095	1100
Arg Pro Asp Gly His Ser Ala Cys Arg Arg Leu Ala Gln Ala Gln Ser		
1105	1110	1115
Met Cys Leu Pro Ile Tyr Arg Glu Ala Cys Gln Glu Gly Glu Gln Ala		
1125	1130	1135
Gly Ala Pro Ala Trp Gln His Arg Gln His Val Cys Leu His Ala His		
1140	1145	1150
Ala His Leu Pro Leu Cys Trp Gly Ala Val Cys Pro His Leu Pro Pro		
1155	1160	1165
Cys Asp Ser His Gly Ser Trp Leu Ser Gly Ala Trp Gly Pro Leu Gly		
1170	1175	1180
His Ser Gly Arg Thr Leu Gly Leu Gly Thr Gly Tyr Arg Asp Ser Gly		
1185	1190	1195
Gly Leu Asp Glu Ile Ser Ser Val Ala Arg Gly Thr Gln Gly Phe Pro		
1205	1210	1215
Gly Pro Cys Thr Trp Arg Arg Ile Ser Ser Leu Glu Ser Glu Val		
1220	1225	1230

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4017 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 189..3848

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

CCCTTAATAA GATTTCACNAC GTACACTCGA GCCATCGCGA GTGTCCTTGA GCGCGGGTG	60
ACGGTGGCTC TCGCTGCTCG CGCCCCCTCC TCCCGCGGGG GGAGCCTGAT GCCACGTTCC	120
CTATGAATTA TTTATCGCCG GCCTAAAAAT ACCCCGAAC TCAACAGCCCC AGTGACCCCTC	180
CGGTGGAC ATG GGT GGG GCC CTG GGG CCG GCC CTG TTG CTC ACC TCG CTC Met Gly Gly Ala Leu Gly Pro Ala Leu Leu Leu Thr Ser Leu	230
1 5 10	
TTC GGT GCC TGG GCA GGG CTG GGT CCG GGG CAG GGC CAG GGC ATG Phe Gly Ala Trp Ala Gly Leu Gly Pro Gly Gln Gly Glu Gln Gly Met	278
15 20 25 30	
ACG GTG GCC GTG GTG TTT AGC AGC TCA GGG CCG CCC CAG GCC CAG TTC Thr Val Ala Val Val Phe Ser Ser Gly Pro Pro Gln Ala Gln Phe	326

35	40	45	
CGT GTC CGC CTT ACT CCC CAG AGC TTC CTG GAC CTA CCC CTG GAG ATC Arg Val Arg Leu Thr Pro Gln Ser Phe Leu Asp Leu Pro Leu Glu Ile 50	55	60	374
CAG CGG CTC ACA GTT GGG GTC AAC ACC ACC AAC CCC AGC AGC CTC CTC Gln Pro Leu Thr Val Gly Val Asn Thr Thr Asn Pro Ser Ser Leu Leu 65	70	75	422
ACC CAG ATC TGC GGC CTC CTG GGT GCT GCC CAC GTC CAC GGC ATT GTC Thr Gln Ile Cys Gly Leu Leu Gly Ala Ala His Val His Gly Ile Val 80	85	90	470
TTT GAG GAC AAC GTG GAC ACC GAG GCG GTG GCC CAG ATC CTT GAC TTC Phe Glu Asp Asn Val Asp Thr Glu Ala Val Ala Gln Ile Leu Asp Phe 95	100	105	518
ATC TCC TCC CAG ACC CAT GTG CCC ATC CTC AGC ATC AGC GGA GGC TCT Ile Ser Ser Gln Thr His Val Pro Ile Leu Ser Ile Ser Gly Gly Ser 115	120	125	566
GCT GTG GTC CTC ACC CCC AAG GAG CCG GGC TCC GCC TTC CTG CAG CTG Ala Val Val Leu Thr Pro Lys Glu Pro Gly Ser Ala Phe Leu Gln Leu 130	135	140	614
GGC GTG TCC CTG GAG CAG CAG CTG CAG GTG CTG TTC AAG GTG CTG GAA Gly Val Ser Leu Glu Gln Gln Leu Gln Val Leu Phe Lys Val Leu Glu 145	150	155	662
GAG TAC GAC TGG AGC GCC TTC GCC GTC ATC ACC AGC CTG CAC CCG GGC Glu Tyr Asp Trp Ser Ala Phe Ala Val Ile Thr Ser Leu His Pro Gly 160	165	170	710
CAC GCG CTC TTC CTG GAG GGC GTG CGC GCC GTC GCC GAC GCG AGC CAC His Ala Leu Phe Leu Glu Gly Val Arg Ala Val Ala Asp Ala Ser His 175	180	185	758
GTG AGT TGG CGG CTG CTG GAC GTG GTC ACG CTG GAA CTG GAC CCG GGA Val Ser Trp Arg Leu Leu Asp Val Val Thr Leu Glu Leu Asp Pro Gly 195	200	205	806
GGG CCG CGC GCG CGC ACG CAG CGC CTG CTG CGC CAG CTC GAC GCG CCC Gly Pro Arg Ala Arg Thr Gln Arg Leu Leu Arg Gln Leu Asp Ala Pro 210	215	220	854
GTG TTT GTG GCC TAC TGC TCG CGC GAG GAG GCC GAG GTG CTC TTC GCC Val Phe Val Ala Tyr Cys Ser Arg Glu Glu Ala Glu Val Leu Phe Ala 225	230	235	902
GAG GCG GCG CAG GCC GGT CTG GTG GGG CCC GGC CAC GTG TGG CTG GTG Glu Ala Ala Gln Ala Gly Leu Val Gly Pro Gly His Val Trp Leu Val 240	245	250	950
CCC AAC CTG GCG CTG GGC AGC ACC GAT GCG CCC CCC GCC ACC TTC CCC Pro Asn Leu Ala Leu Gly Ser Thr Asp Ala Pro Pro Ala Thr Phe Pro 255	260	265	998
GTG GGC CTC ATC AGC GTC GTC ACC GAG AGC TGG CGC CTC AGC CTG CGC Val Gly Leu Ile Ser Val Val Thr Glu Ser Trp Arg Leu Ser Leu Arg 275	280	285	1046
CAG AAG GTG CGC GAC GGC GTG GCC ATT CTG GCC CTG GGC GCG CAC AGC Gln Lys Val Arg Asp Gly Val Ala Ile Leu Ala Leu Gly Ala His Ser 290	295	300	1094
TAC TGG CGC CAG CAT GGA ACC CTG CCA GCC CCG CCC GGG GAC TGC CGT			1142

Tyr Trp Arg Gln His Gly Thr Leu Pro Ala Pro Ala Gly Asp Cys Arg		
305	310	315
GTT CAT CCT GGG CCC GTC AGC CCT GCC CGG GAG GCC TTC TAC AGG CAC		1190
Val His Pro Gly Pro Val Ser Pro Ala Arg Glu Ala Phe Tyr Arg His		
320	325	330
CTA CTG AAT GTC ACC TGG GAG GGC CGA GAC TTC TCC TTC AGC CCT GGT		1238
Leu Leu Asn Val Thr Trp Glu Gly Arg Asp Phe Ser Phe Ser Pro Gly		
335	340	345
350		
GGG TAC CTG GTC CAG CCC ACC ATG GTG GTG ATC GCC CTC AAC CGG CAC		1286
Gly Tyr Leu Val Gln Pro Thr Met Val Val Ile Ala Leu Asn Arg His		
355	360	365
CGC CTC TGG GAG ATG GTG GGG CGC TGG GAG CAT GGC GTC CTA TAC ATG		1334
Arg Leu Trp Glu Met Val Gly Arg Trp Glu His Gly Val Leu Tyr Met		
370	375	380
AAG TAC CCC GTG TGG CCT CGC TAC AGT GCC TCT CTG CAG CCT GTG GTG		1382
Lys Tyr Pro Val Trp Pro Arg Tyr Ser Ala Ser Leu Gln Pro Val Val		
385	390	395
GAC AGT CGG CAC CTG ACG GTG GCC ACG CTG GAA GAG CGG CCC TTT GTC		1430
Asp Ser Arg His Leu Thr Val Ala Thr Leu Glu Glu Arg Pro Phe Val		
400	405	410
ATC GTG GAG AGC CCT GAC CCT GGC ACA GGA GGC TGT GTC CCC AAC ACC		1478
Ile Val Glu Ser Pro Asp Pro Gly Thr Gly Gly Cys Val Pro Asn Thr		
415	420	425
430		
GTG CCC TGC CGC AGG CAG AGC AAC CAC ACC TTC AGC AGC GGG GAC GTG		1526
Val Pro Cys Arg Arg Gln Ser Asn His Thr Phe Ser Ser Gly Asp Val		
435	440	445
GCC CCC TAC ACC AAG CTC TGC TGT AAG GGA TTC TGC ATC GAC ATC CTC		1574
Ala Pro Tyr Thr Lys Leu Cys Cys Lys Gly Phe Cys Ile Asp Ile Leu		
450	455	460
AAG AAG CTG GCC AGA GTG GTC AAA TTC TCC TAC GAC CTG TAC CTG GTG		1622
Lys Lys Leu Ala Arg Val Val Lys Phe Ser Tyr Asp Leu Tyr Leu Val		
465	470	475
ACC AAC GGC AAG CAT GGC AAG CGG GTG CGC GGC GTA TGG AAC GGC ATG		1670
Thr Asn Gly Lys His Gly Lys Arg Val Arg Gly Val Trp Asn Gly Met		
480	485	490
ATT GGG GAG GTG TAC TAC AAG CGG GCA GAC ATG GCC ATC GGC TCC CTC		1718
Ile Gly Glu Val Tyr Tyr Lys Arg Ala Asp Met Ala Ile Gly Ser Leu		
495	500	505
510		
ACC ATC AAT GAG GAA CGC TCC GAG ATC GTA GAC TTC TCT GTA CCC TTT		1766
Thr Ile Asn Glu Glu Arg Ser Glu Ile Val Asp Phe Ser Val Pro Phe		
515	520	525
GTG GAG ACG GGC ATC AGT GTG ATG GTG GCT CGC AGC AAT GGC ACC GTC		1814
Val Glu Thr Gly Ile Ser Val Met Val Ala Arg Ser Asn Gly Thr Val		
530	535	540
TCC CCC TCG GCC TTC TTG GAG CCA TAT AGC CCT GCA GTG TGG GTG ATG		1862
Ser Pro Ser Ala Phe Leu Glu Pro Tyr Ser Pro Ala Val Trp Val Met		
545	550	555
ATG TTT GTC ATG TGC CTC ACT GTG GTG GCC ATC ACC GTC TTC ATG TTC		1910
Met Phe Val Met Cys Leu Thr Val Val Ala Ile Thr Val Phe Met Phe		
560	565	570

GAG TAC TTC AGC CCT GTC AGC TAC AAC CAG AAC CTC ACC AGA GGC AAG Glu Tyr Phe Ser Pro Val Ser Tyr Asn Gln Asn Leu Thr Arg Gly Lys 575 580 585 590	1958
AAG TCC GGG GGC CCA GCT TTC ACT ATC GGC AAG TCC GTG TGG CTG CTG Lys Ser Gly Gly Pro Ala Phe Thr Ile Gly Lys Ser Val Trp Leu Leu 595 600 605	2006
TGG GCG CTG GTC TTC AAC AAC TCA GTG CCC ATC GAG AAC CCG CGG GGC Trp Ala Leu Val Phe Asn Asn Ser Val Pro Ile Glu Asn Pro Arg Gly 610 615 620	2054
ACC ACC AGC AAG ATC ATG GTT CTG GTC TGG GCC TTC TTT GCT GTC ATC Thr Thr Ser Lys Ile Met Val Leu Val Trp Ala Phe Ala Val Ile 625 630 635	2102
TTC CTC GCC AGA TAC ACG GCC AAC CTG GCC GCC TTC ATG ATC CAA GAG Phe Leu Ala Arg Tyr Thr Ala Asn Leu Ala Phe Met Ile Gln Glu 640 645 650	2150
CAA TAC ATC GAC ACT GTG TCG GGC CTC AGT GAC AAG AAG TTT CAG CGG Gln Tyr Ile Asp Thr Val Ser Gly Leu Ser Asp Lys Lys Phe Gln Arg 655 660 665 670	2198
CCT CAA GAT CAG TAC CCA CCT TTC CGC TTC GGC ACG GTG CCC AAC GGC Pro Gln Asp Gln Tyr Pro Pro Phe Arg Phe Gly Thr Val Pro Asn Gly 675 680 685	2246
AGC ACG GAG CGG AAC ATC CGC AGT AAC TAC CGT GAC ATG CAC ACC CAC Ser Thr Glu Arg Asn Ile Arg Ser Asn Tyr Arg Asp Met His Thr His 690 695 700	2294
ATG GTC AAG TTC AAC CAG CGC TCG GTG GAG GAC GCG CTC ACC AGC CTC Met Val Lys Phe Asn Gln Arg Ser Val Glu Asp Ala Leu Thr Ser Leu 705 710 715	2342
AAG ATG GGC AAG GAC GAG GGC TGC AAG CTG GTC ACC ATT GGG TCT GGC Lys Met Gly Lys Asp Glu Gly Cys Lys Leu Val Thr Ile Gly Ser Gly 720 725 730	2390
AAG GTC TTT GCT ACC ACT GGC TAC GGC ATC GCC ATG CAG AAG GAC TCC Lys Val Phe Ala Thr Thr Gly Tyr Gly Ile Ala Met Gln Lys Asp Ser 735 740 745 750	2438
CAC TGG AAG CGG GCC ATA GAC CTG GCG CTC TTG CAG TTC CTG GGG GAC His Trp Lys Arg Ala Ile Asp Leu Ala Leu Leu Gln Phe Leu Gly Asp 755 760 765	2486
GGA GAG ACA CAG AAA CTG GAG ACA GTG TGG CTC TCA GGG ATC TGC CAG Gly Glu Thr Gln Lys Leu Glu Thr Val Trp Leu Ser Gly Ile Cys Gln 770 775 780	2534
AAT GAG AAG AAC GAG GTG ATG AGC AGC AAG CTG GAC ATC GAC AAC ATG Asn Glu Lys Asn Glu Val Met Ser Ser Lys Leu Asp Ile Asp Asn Met 785 790 795	2582
GGA GGC GTC TTC TAC ATG CTG CTG GTG GCC ATG GGG CTG GCC CTG CTG Gly Gly Val Phe Tyr Met Leu Leu Val Ala Met Gly Leu Ala Leu Leu 800 805 810	2630
GTC TTC GCC TGG GAG CAC CTG GTC TAC TGG AAG CTG CGC CAC TCG GTG Val Phe Ala Trp Glu His Leu Val Tyr Trp Lys Leu Arg His Ser Val 815 820 825 830	2678
CCC AAC TCA TCC CAG CTG GAC TTC CTG CTG GCT TTC AGC AGG GGC ATC Pro Asn Ser Ser Gln Leu Asp Phe Leu Leu Ala Phe Ser Arg Gly Ile 835 840 845	2726

TAC AGC TGC TTC AGC GGG GTG CAG AGC CTC GCC AGC CCA CGG CGG CAG Tyr Ser Cys Phe Ser Gly Val Gln Ser Leu Ala Ser Pro Pro Arg Gln 850 855 860	2774
GCT AGC CCG GAC CTC ACG GCT AGC TCG GCC CAG GCC AGC GTG CTC AAG Ala Ser Pro Asp Leu Thr Al Ser Ser Ala Gln Ala Ser Val Leu Lys 865 870 875	2822
ATT CTG CAG GCA GCC CGC GAC ATG GTG ACC ACG GCG GGC GTA AGC AAC Ile Leu Gln Ala Ala Arg Asp Met Val Thr Thr Ala Gly Val Ser Asn 880 885 890	2870
TCC CTG GAC CGC GCC ACT CGC ACC ATC GAG AAT TGG GGT GGC GGC CGC Ser Leu Asp Arg Ala Thr Arg Thr Ile Glu Asn Trp Gly Gly Gly Arg 895 900 905 910	2918
CGT GCG CCC CCA CCG TCC CCC TGC CCG ACC CCG CGG TCT GGC CCC AGC Arg Ala Pro Pro Pro Ser Pro Cys Pro Thr Pro Arg Ser Gly Pro Ser 915 920 925	2966
CCA TGC CTG CCC ACC CCC GAC CCG CCC CCA GAG CCG AGC CCC ACG GGC Pro Cys Leu Pro Thr Pro Asp Pro Pro Pro Glu Pro Ser Pro Thr GLY 930 935 940	3014
TGG GGA CCG CCA GAC GGG GGT CGC GCG GCG CTT GTG CGC AGG GCT CCG Trp Gly Pro Pro Asp Gly Gly Arg Ala Ala Leu Val Arg Arg Ala Pro 945 950 955	3062
CAG CCC CCG GGC CGC CCC CCG ACG CCG GGG CCG CCC CTG TCC GAC GTC Gln Pro Pro Gly Arg Pro Pro Thr Pro Gly Pro Pro Leu Ser Asp Val 960 965 970	3110
TCC CGA GTG TCG CGC CGC CCA GCC TGG GAG GCG CGG TGG CCG GTG CGG Ser Arg Val Ser Arg Arg Pro Ala Trp Glu Ala Arg Trp Pro Val Arg 975 980 985 990	3158
ACC GGG CAC TGC GGG AGG CAC CTC TCG GCC TCC GAG CGG CCC CTG TCG Thr Gly His Cys Gly Arg His Leu Ser Ala Ser Glu Arg Pro Leu Ser 995 1000 1005	3206
CCC GCG CGC TGT CAC TAC AGC TCC TTT CCT CGA GCC GAC CGA TCC GGC Pro Ala Arg Cys His Tyr Ser Ser Phe Pro Arg Ala Asp Arg Ser Gly 1010 1015 1020	3254
CGC CCC TTC CTC CCG CTC TTC CCG GAG CCC CCG GAG CTG GAG GAC CTG Arg Pro Phe Leu Pro Leu Phe Pro Glu Pro Pro Glu Leu Glu Asp Leu 1025 1030 1035	3302
CGG CTG CTC GGT CCG GAG CAG CTG GCC CGG CGG GAG GCC CTG CTG AAC Pro Leu Leu Gly Pro Glu Gln Leu Ala Arg Arg Glu Ala Leu Leu Asn 1040 1045 1050	3350
GCG GCC TGG GCC CGG GGC TCG CGC CCG AGT CAC GCT TCC CTG CCC AGC Ala Ala Trp Ala Arg Gly Ser Arg Pro Ser His Ala Ser Leu Pro Ser 1055 1060 1065 1070	3398
TCC GTG GCC GAG GCC TTC GCT CGG CCC AGC TCG CTG CCC GCT GGG TGC Ser Val Ala Glu Ala Phe Ala Arg Pro Ser Ser Leu Pro Ala Gly Cys 1075 1080 1085	3446
ACC GGC CCC GCC TGC GCC CGC CCC GAC GGC CAC TCG GCC TGC AGG CGC Thr Gly Pro Ala Cys Ala Arg Pro Asp Gly His Ser Ala Cys Arg Arg 1090 1095 1100	3494
TTG GCG CAG GCG CAG TCG ATG TGC TTG CCG ATC TAC CGG GAG GCC TGC Leu Ala Gln Ala Gln Ser Met Cys Leu Pro Ile Tyr Arg Glu Ala Cys 1105 1110 1115	3542

CAG GAG GGC GAG CAG GCA GGG GCC CCC GCC TGG CAG CAC AGA CAG CAC Gln Glu Gly Glu Gln Ala Gly Ala Pro Ala Trp Gln His Arg Gln His 1120 1125 1130	3590
GTC TGC CTG CAC GCC CAC GGC CAC CTG CCA TTG TGC TGG GGG GCT GTC Val Cys Leu His Ala His Ala His Leu Pro Leu Cys Trp Gly Ala Val 1135 1140 1145 1150	3638
TGT CCT CAC CTT CCC TGT GAC AGC CAC GGC TCC TGG CTC TCC GGC Cys Pro His Leu Pro Pro Cys Asp Ser His Gly Ser Trp Leu Ser Gly 1155 1160 1165	3686
GCC TGG GGG CCT CTG GGG CAC AGC GGC AGG ACT CTG GGG CTG GGC ACA Ala Trp Gly Pro Leu Gly His Ser Gly Arg Thr Leu Gly Leu Gly Thr 1170 1175 1180	3734
GGC TAC AGA GAC AGT GGG GGA CTG GAC GAG ATC AGC AGT GTA GCC CGT Gly Tyr Arg Asp Ser Gly Gly Leu Asp Glu Ile Ser Ser Val Ala Arg 1185 1190 1195	3782
GGG ACG CAA GGC TTC CCG GGA CCC TGC ACC TGG AGA CGG ATC TCC AGT Gly Thr Gln Gly Phe Pro Gly Pro Cys Thr Trp Arg Arg Ile Ser Ser 1200 1205 1210	3830
CTG GAG TCA GAA GTG TGAGTTATCA GCCACTCAGG CTCCGAGCCA GCTGGATTCT Leu Glu Ser Glu Val 1215 122	3885
CTGCCTGCCA CTGTCAGGGT TAAGCGGCAG GCAGGATTGG CCCTTCTCTG GCTTCTACCA TGAAATCCTG GCCATGGCAC CCCAGTGACA GATGATGTCT TCCATGGTCA TCAGTGACCT CAGCTAGCCT CA	3945 4005 4017

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1219 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

Met Gly Gly Ala Leu Gly Pro Ala Leu Leu Leu Thr Ser Leu Phe Gly 1 5 10 15
Ala Trp Ala Gly Leu Gly Pro Gly Gln Gly Glu Gln Gly Met Thr Val 20 25 30
Ala Val Val Phe Ser Ser Ser Gly Pro Pro Gln Ala Gln Phe Arg Val 35 40 45
Arg Leu Thr Pro Gln Ser Phe Leu Asp Leu Pro Leu Glu Ile Gln Pro 50 55 60
Leu Thr Val Gly Val Asn Thr Thr Asn Pro Ser Ser Leu Leu Thr Gln 65 70 75 80
Ile Cys Gly Leu Leu Gly Ala Ala His Val His Gly Ile Val Phe Glu 85 90 95
Asp Asn Val Asp Thr Glu Ala Val Ala Gln Ile Leu Asp Phe Ile Ser 100 105 110

Ser Gln Thr His Val Pro Ile Leu Ser Ile Ser Gly Gly Ser Ala Val
115 120 125

Val Leu Thr Pro Lys Glu Pro Gly Ser Ala Phe Leu Gln Leu Gly Val
130 135 140

Ser Leu Glu Gln Gln Leu Gin Val Leu Phe Lys Val Leu Glu Glu Tyr
145 150 155 160

Asp Trp Ser Ala Phe Ala Val Ile Thr Ser Leu His Pro Gly His Ala
165 170 175

Leu Phe Leu Glu Gly Val Arg Ala Val Ala Asp Ala Ser His Val Ser
180 185 190

Trp Arg Leu Leu Asp Val Val Thr Leu Glu Leu Asp Pro Gly Gly Pro
195 200 205

Arg Ala Arg Thr Gln Arg Leu Leu Arg Gln Leu Asp Ala Pro Val Phe
210 215 220

Val Ala Tyr Cys Ser Arg Glu Glu Ala Glu Val Leu Phe Ala Glu Ala
225 230 235 240

Ala Gln Ala Gly Leu Val Gly Pro Gly His Val Trp Leu Val Pro Asn
245 250 255

Leu Ala Leu Gly Ser Thr Asp Ala Pro Pro Ala Thr Phe Pro Val Gly
260 265 270

Leu Ile Ser Val Val Thr Glu Ser Trp Arg Leu Ser Leu Arg Gln Lys
275 280 285

Val Arg Asp Gly Val Ala Ile Leu Ala Leu Gly Ala His Ser Tyr Trp
290 295 300

Arg Gln His Gly Thr Leu Pro Ala Pro Ala Gly Asp Cys Arg Val His
305 310 315 320

Pro Gly Pro Val Ser Pro Ala Arg Glu Ala Phe Tyr Arg His Leu Leu
325 330 335

Asn Val Thr Trp Glu Gly Arg Asp Phe Ser Phe Ser Pro Gly Gly Tyr
340 345 350

Leu Val Gln Pro Thr Met Val Val Ile Ala Leu Asn Arg His Arg Leu
355 360 365

Trp Glu Met Val Gly Arg Trp Glu His Gly Val Leu Tyr Met Lys Tyr
370 375 380

Pro Val Trp Pro Arg Tyr Ser Ala Ser Leu Gln Pro Val Val Asp Ser
385 390 395 400

Arg His Leu Thr Val Ala Thr Leu Glu Glu Arg Pro Phe Val Ile Val
405 410 415

Glu Ser Pro Asp Pro Gly Thr Gly Gly Cys Val Pro Asn Thr Val Pro
420 425 430

Cys Arg Arg Gln Ser Asn His Thr Phe Ser Ser Gly Asp Val Ala Pro
435 440 445

Tyr Thr Lys Leu Cys Cys Lys Gly Phe Cys Ile Asp Ile Leu Lys Lys
450 455 460

Leu Ala Arg Val Val Lys Phe Ser Tyr Asp Leu Tyr Leu Val Thr Asn

465 470 475 480
Gly Lys His Gly Lys Arg Val Arg Gly Val Trp Asn Gly Met Ile Gly
485 490 495
Glu Val Tyr Tyr Lys Arg Ala Asp Met Ala Ile Gly Ser Leu Thr Ile
500 505 510
Asn Glu Glu Arg Ser Glu Ile Val Asp Phe Ser Val Pro Phe Val Glu
515 520 525
Thr Gly Ile Ser Val Met Val Ala Arg Ser Asn Gly Thr Val Ser Pro
530 535 540
Ser Ala Phe Leu Glu Pro Tyr Ser Pro Ala Val Trp Val Met Met Phe
545 550 555 560
Val Met Cys Leu Thr Val Val Ala Ile Thr Val Phe Met Phe Glu Tyr
565 570 575
Phe Ser Pro Val Ser Tyr Asn Gln Asn Leu Thr Arg Gly Lys Lys Ser
580 585 590
Gly Gly Pro Ala Phe Thr Ile Gly Lys Ser Val Trp Leu Leu Trp Ala
595 600 605
Leu Val Phe Asn Asn Ser Val Pro Ile Glu Asn Pro Arg Gly Thr Thr
610 615 620
Ser Lys Ile Met Val Leu Val Trp Ala Phe Phe Ala Val Ile Phe Leu
625 630 635 640
Ala Arg Tyr Thr Ala Asn Leu Ala Ala Phe Met Ile Gln Glu Gln Tyr
645 650 655

Ile Asp Thr Val Ser Gly Leu Ser Asp Lys Lys Phe Gln Arg Pro Gln
660 665 670
Asp Gln Tyr Pro Pro Phe Arg Phe Gly Thr Val Pro Asn Gly Ser Thr
675 680 685
Glu Arg Asn Ile Arg Ser Asn Tyr Arg Asp Met His Thr His Met Val
690 695 700
Lys Phe Asn Gln Arg Ser Val Glu Asp Ala Leu Thr Ser Leu Lys Met
705 710 715 720
Gly Lys Asp Glu Gly Cys Lys Leu Val Thr Ile Gly Ser Gly Lys Val
725 730 735
Phe Ala Thr Thr Gly Tyr Gly Ile Ala Met Gln Lys Asp Ser His Trp
740 745 750
Lys Arg Ala Ile Asp Leu Ala Leu Leu Gln Phe Leu Gly Asp Gly Glu
755 760 765
Thr Gln Lys Leu Glu Thr Val Trp Leu Ser Gly Ile Cys Gln Asn Glu
770 775 780
Lys Asn Glu Val Met Ser Ser Lys Leu Asp Ile Asp Asn Met Gly Gly
785 790 795 800
Val Phe Tyr Met Leu Leu Val Ala Met Gly Leu Ala Leu Leu Val Phe
805 810 815
Ala Trp Glu His Leu Val Tyr Trp Lys Leu Arg His Ser Val Pro Asn

820	825	830	
Ser Ser Gin Leu Asp Phe Leu Leu Ala Phe Ser Arg Gly Ile Tyr Ser			
835	840	845	
Cys Phe Ser Gly Val Gln Ser Leu Ala Ser Pro Pro Arg Gln Ala Ser			
850	855	860	
Pro Asp Leu Thr Ala Ser Ser Ala Gln Ala Ser Val Leu Lys Ile Leu			
865	870	880	
Gln Ala Ala Arg Asp Met Val Thr Thr Ala Gly Val Ser Asn Ser Leu			
885	890	895	
Asp Arg Ala Thr Arg Thr Ile Glu Asn Trp Gly Gly Arg Arg Ala			
900	905	910	
Pro Pro Pro Ser Pro Cys Pro Thr Pro Arg Ser Gly Pro Ser Pro Cys			
915	920	925	
Leu Pro Thr Pro Asp Pro Pro Glu Pro Ser Pro Thr Gly Trp Gly			
930	935	940	
Pro Pro Asp Gly Gly Arg Ala Ala Leu Val Arg Arg Ala Pro Gln Pro			
945	950	955	960
Pro Gly Arg Pro Pro Thr Pro Gly Pro Pro Leu Ser Asp Val Ser Arg			
965	970	975	
Val Ser Arg Arg Pro Ala Trp Glu Ala Arg Trp Pro Val Arg Thr Gly			
980	985	990	
His Cys Gly Arg His Leu Ser Ala Ser Glu Arg Pro Leu Ser Pro Ala			
995	1000	1005	
Arg Cys His Tyr Ser Ser Phe Pro Arg Ala Asp Arg Ser Gly Arg Pro			
1010	1015	1020	
Phe Leu Pro Leu Phe Pro Glu Pro Pro Glu Leu Glu Asp Leu Pro Leu			
1025	1030	1035	1040
Leu Gly Pro Glu Gln Leu Ala Arg Arg Glu Ala Leu Leu Asn Ala Ala			
1045	1050	1055	
Trp Ala Arg Gly Ser Arg Pro Ser His Ala Ser Leu Pro Ser Ser Val			
1060	1065	1070	
Ala Glu Ala Phe Ala Arg Pro Ser Ser Leu Pro Ala Gly Cys Thr Gly			
1075	1080	1085	
Pro Ala Cys Ala Arg Pro Asp Gly His Ser Ala Cys Arg Arg Leu Ala			
1090	1095	1100	
Gln Ala Gln Ser Met Cys Leu Pro Ile Tyr Arg Glu Ala Cys Gln Glu			
1105	1110	1115	1120
Gly Glu Gln Ala Gly Ala Pro Ala Trp Gln His Arg Gln His Val Cys			
1125	1130	1135	
Leu His Ala His Ala His Leu Pro Leu Cys Trp Gly Ala Val Cys Pro			
1140	1145	1150	
His Leu Pro Pro Cys Asp Ser His Gly Ser Trp Leu Ser Gly Ala Trp			
1155	1160	1165	
Gly Pro Leu Gly His Ser Gly Arg Thr Leu Gly Leu Gly Thr Gly Tyr			

1170 1175 1180
Arg Asp Ser Gly Gly Leu Asp Glu Ile Ser Ser Val Ala Arg Gly Thr
1185 1190 1195 1200
Gln Gly Phe Pro Gly Pro Cys Thr Trp Arg Arg Ile Ser Ser Leu Glu
1205 1210 1215
Ser Glu Val

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4077 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 189..3908

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

CCCTTAATAA GATTTGCNAC GTACACTCGA GCCATCGCGA GTGTCCTTGA GCGCGGGTG	60
ACGGTGGCTC TCGCTGCTCG CGCCCCCTCC TCCCAGGGGG GGAGCCTGAT GCCACGTTCC	120
CTATGAATTA TTTATC3CCG GCCTAAAAAT ACCCCGAACT TCACAGCCCG AGTGACCCCTC	180
CGGTGGAC ATG GGT GGG GCC CTG GGG CCG GCC CTG TTG CTC ACC TCG CTC Met Gly Ala Leu Gly Pro Ala Leu Leu Thr Ser Leu	230
1 5 10	
TTC GGT GCC TGG GCA GGG CTG GGT CCG GGG CAG GGC GAG CAG GGC ATG Phe Gly Ala Trp Ala Gly Leu Gly Pro Gly Gln Gly Glu Gln Gly Met	278
15 20 25 30	
ACG GTG GCC GTG GTG TTT AGC AGC TCA GGG CCG CCC CAG GCC CAG TTC Thr Val Ala Val Val Phe Ser Ser Gly Pro Pro Gln Ala Gln Phe	326
35 40 45	
CGT GTC CGC CTC ACC CCC CAG AGC TTC CTG GAC CTA CCC CTG GAG ATC Arg Val Arg Leu Thr Pro Gln Ser Phe Leu Asp Leu Pro Leu Glu Ile	374
50 55 60	
CAG CCG CTC ACA GTT GGG GTC AAC ACC ACC AAC CCC AGC AGC CTC CTC Gln Pro Leu Thr Val Gly Val Asn Thr Thr Asn Pro Ser Ser Leu Leu	422
65 70 75	
ACC CAG ATC TGC GGC CTC CTG GGT GCT GCC CAC GTC CAC GGC ATT GTC Thr Gln Ile Cys Gly Leu Leu Gly Ala Ala His Val His Gly Ile Val	470
80 85 90	
TTT GAG GAC AAC GTG GAC ACC GAG GCG GTG GCC CAG ATC CTT GAC TTC Phe Glu Asp Asn Val Asp Thr Glu Ala Val Ala Gln Ile Leu Asp Phe	518
95 100 105 110	
ATC TCC TCC CAG ACC CAT GTG CCC ATC CTC AGC ATC AGC GGA GGC TCT Ile Ser Ser Gln Thr His Val Pro Ile Leu Ser Ile Ser Gly Gly Ser	566
115 120 125	

GCT GTG GTC CTC ACC CCC AAG GAG CCG GGC TCC GCC TTC CTG CAG CTG Ala Val Val Leu Thr Pro Lys Glu Pro Gly Ser Ala Phe Leu Gln Leu 130 135 140	614
GGC GTG TCC CTG GAA CAG CAG CTG CAG GTG CTG TTC AAG GTG CTG GAA Gly Val Ser Leu Glu Gin Gln Leu Gln Val Leu Phe Lys Val Leu Glu 145 150 155	662
GAG TAC GAC TGG AGC GCC TTC GCC GTC ATC ACC AGC CTG CAC CCG GGC Glu Tyr Asp Trp Ser Ala Phe Ala Val Ile Thr Ser Leu His Pro Gly 160 165 170	710
CAC GCG CTC TTC CTG GAG GGC GTG CGC GCC GTC GCC GAC GCC AGC CAC His Ala Leu Phe Leu Glu Gly Val Arg Ala Val Ala Asp Ala Ser His 175 180 185 190	758
GTG AGT TGG CGG CTG CTG GAC GTG GTC ACG CTG GAA CTG GAC CCG GGA Val Ser Trp Arg Leu Leu Asp Val Val Thr Leu Glu Leu Asp Pro Gly 195 200 205	806
GGG CCG CGC GCG CGC ACG CAG CGC CTG CTG CGC CAG CTC GAC GCG CCC Gly Pro Arg Ala Arg Thr Gln Arg Leu Leu Arg Gln Leu Asp Ala Pro 210 215 220	854
GTG TTT GTG GCC TAC TGC TCG CGC GAG GAG GCC GAG GTG CTC TTC GCC Val Phe Val Ala Tyr Cys Ser Arg Glu Glu Ala Glu Val Leu Phe Ala 225 230 235	902
GAG GCG GCG CAG GCC GGT CTG GTG GGG CCC GGC CAC GTG TGG CTG GTG Glu Ala Ala Gln Ala Gly Leu Val Gly Pro Gly His Val Trp Leu Val 240 245 250	950
CCC AAC CTG GCG CTG GGC AGC ACC GAT GCG CCC CCC GCC ACC TTC CCC Pro Asn Leu Ala Leu Gly Ser Thr Asp Ala Pro Pro Ala Thr Phe Pro 255 260 265 270	998
GTG GGC CTC ATC AGC GTC GTG ACC GAG AGC TGG CGC CTC AGC CTG CGC Val Gly Leu Ile Ser Val Val Thr Glu Ser Trp Arg Leu Ser Leu Arg 275 280 285	1046
CAG AAG GTG CGC GAC GGC GTG GCC ATT CTG GCC CTG GGC GCC CAC AGC Gln Lys Val Arg Asp Gly Val Ala Ile Leu Ala Leu Gly Ala His Ser 290 295 300	1094
TAC TGG CGC CAG CAT GGA ACC CTG CCA GCC CCG GCC GGG GAC TGC CGT Tyr Trp Arg Gln His Gly Thr Leu Pro Ala Pro Ala Gly Asp Cys Arg 305 310 315	1142
GTT CAC CCT GGG CCC GTC AGC CCT GCC CGG GAG GCC TTC TAC AGG CAC Val His Pro Gly Pro Val Ser Pro Ala Arg Glu Ala Phe Tyr Arg His 320 325 330	1190
CTA CTG AAT GTC ACC TGG GAS GGC CGA GAC TTC TCC TTC AGC CCT GGT Leu Leu Asn Val Thr Trp Glu Gly Arg Asp Phe Ser Phe Ser Pro Gly 335 340 345 350	1238
GGG TAC CTG GTC CAG CCC ACC ATG GTG GTG ATC GCC CTC AAC CGG CAC Gly Tyr Leu Val Gln Pro Thr Met Val Val Ile Ala Leu Asn Arg His 355 360 365	1286
CGC CTC TGG GAG ATG GTG GGG CGC TGG GAG CAT GGC GTC CTA TAC ATG Arg Leu Trp Glu Met Val Gly Arg Trp Glu His Gly Val Leu Tyr Met 370 375 380	1334
AAG TAC CCC GTG TGG CCT CGC TAC AGT GGC TCT CTG CAG CCT GTG GTG Lys Tyr Pro Val Trp Pro Arg Tyr Ser Ala Ser Leu Gln Pro Val Val 385 390 395	1382

GAC AGT CGG CAC CTG ACG GTG GCC ACG CTG GAA GAG CGG CCC TTT GTC	1430
Asp Ser Arg His Leu Thr Val Ala Thr Leu Glu Arg Pro Phe Val	
400 405 410	
ATC GTG GAG AGC CCT GAC CCT GGC ACA GGA GGC TGT GTC CCC AAC ACG	1478
Ile Val Glu Ser Pro Asp Pro Gly Thr Gly Gly Cys Val Pro Asn Thr	
415 420 425 430	
GTG CCC TGC CGC AGG CAG AGC AAC CAC ACC TTC AGC AGC GGG GAC GTG	1526
Val Pro Cys Arg Arg Gln Ser Asn His Thr Phe Ser Ser Gly Asp Val	
435 440 445	
GCC CCC TAC ACC AAG CTC TGC TGT AAG GGA TTC TGC ATC GAC ATC CTC	1574
Ala Pro Tyr Thr Lys Leu Cys Cys Lys Gly Phe Cys Ile Asp Ile Leu	
450 455 460	
AAG AAG CTG GCC AGA GTG GTC AAA TTC TCC TAC GAC CTG TAC CTG GTG	1622
Lys Lys Leu Ala Arg Val Val Lys Phe Ser Tyr Asp Leu Tyr Leu Val	
465 470 475	
ACC AAC GGC AAG CAT GGC AAG CGG GTG CGC GGC GTA TGG AAC GGC ATG	1670
Thr Asn Gly Lys His Gly Lys Arg Val Arg Gly Val Trp Asn Gly Met	
480 485 490	
ATT GGG GAG GTG TAC TAC AAG CGG GCA GAC ATG GCC ATC GGC TCC CTC	1718
Ile Gly Glu Val Tyr Tyr Lys Arg Ala Asp Met Ala Ile Gly Ser Leu	
495 500 505 510	
ACC ATC AAT GAG GAA CGC TCC GAG ATC GTA GAC TTC TCT GTA CCC TTT	1766
Thr Ile Asn Glu Glu Arg Ser Glu Ile Val Asp Phe Ser Val Pro Phe	
515 520 525	
GTG GAG ACG GGC ATC AGT GTG ATG GTG GCT CGC AGC AAT GGC ACC GTC	1814
Val Glu Thr Ile Ser Val Met Val Ala Arg Ser Asn Gly Thr Val	
530 535 540	
TCC CCC TCG GCC TTC TTG GAG CCA TAT AGC CCT GCA GTG TGG GTG ATG	1862
Ser Pro Ser Ala Phe Leu Glu Pro Tyr Ser Pro Ala Val Trp Val Met	
545 550 555	
ATG TTT GTC ATG TGC CTC ACT GTG GTG GCC ATC ACC GTC TTC ATG TTC	1910
Met Phe Val Met Cys Leu Thr Val Val Ala Ile Thr Val Phe Met Phe	
560 565 570	
GAG TAC TTC AGC CCT GTC AGC TAC AAC CAG AAC CTC ACC AGA GGC AAG	1958
Glu Tyr Phe Ser Pro Val Ser Tyr Asn Gln Asn Leu Thr Arg Gly Lys	
575 580 585 590	
ACT TTC ACT ATC GGC AAG TCC GTG TGG CTG CTG TGG GCG CTG GTC TTC	2006
Thr Phe Thr Ile Gly Lys Ser Val Trp Leu Leu Trp Ala Leu Val Phe	
595 600 605	
AAC AAC TCA GTG CCC ATC GAG AAC CCG CGG GGC ACC ACC AGC AAG ATC	2054
Asn Asn Ser Val Pro Ile Glu Asn Pro Arg Gly Thr Thr Ser Lys Ile	
610 615 620	
ATG GTT CTG GTC TGG GCC TTC TTT GCT GTC ATC TTC CTC GCC AGA TAC	2102
Met Val Leu Val Trp Ala Phe Phe Ala Val Ile Phe Leu Ala Arg Tyr	
625 630 635	
ACG GCC AAC CTG GCC GCC TTC ATG ATC CAA GAG CAA TAC ATC GAC ACT	2150
Thr Ala Asn Leu Ala Ala Phe Met Ile Gln Glu Gln Tyr Ile Asp Thr	
640 645 650	
GTG TCG GGC CTC AGT GAC AAG AAG TTT CAG CGG CCT CAA GAT CAG TAC	2198
Val Ser Gly Leu Ser Asp Lys Lys Phe Gln Arg Pro Gln Asp Gln Tyr	
655 660 665 670	

CCA CCT TTC CGC TTC GGC ACG GTG CCC AAC GGC AGC ACG GAG CGG AAC Pro Pro Phe Arg Phe Gly Thr Val Pro Asn Gly Ser Thr Glu Arg Asn 675 680 685	2246
ATC CGC AGT AAC TAC CGT GAC ATG CAC ACC CAA ATG GTC AAG TTC AAC Ile Arg Ser Asn Tyr Arg Asp Met His Thr His Met Val Lys Phe Asn 690 695 700	2294
CAG CGT TCG GTG GAG GAC GCG CTC ACC AGC CTC AAG ATG GGC TCT GAG Gln Arg Ser Val Glu Asp Ala Leu Thr Ser Leu Lys Met Gly Ser Glu 705 710 715	2342
GCT CAG CCT GTC CCC AGG AAG CTG GAT GCC TTC ATC TAT GAT GCT GCT Ala Gln Pro Val Pro Arg Lys Leu Asp Ala Phe Ile Tyr Asp Ala Ala 720 725 730	2390
GTC CTC AAC TAC ATG GCA GGC AAG GAC GAG GGC TGC AAG CTG GTC ACC Val Leu Asn Tyr Met Ala Gly Lys Asp Glu Gly Cys Lys Leu Val Thr 735 740 745 750	2438
ATT GGG TCT GGC AAG GTC TTT GCT ACC ACT GGC TAC GGC ATC GCC ATG Ile Gly Ser Gly Lys Val Phe Ala Thr Thr Gly Tyr Gly Ile Ala Met 755 760 765	2486
CAG AAG GAC TCC CAC TGG AAG CGG GCC ATA GAC CTG GCG CTC TTG CAG Gln Lys Asp Ser His Trp Lys Arg Ala Ile Asp Leu Ala Leu Leu Gln 770 775 780	2534
TTC CTG GGG GAC GGA GAG ACA CAG AAA CTG GAG ACA GTG TGG CTC TCA Phe Leu Gly Asp Gly Glu Thr Gln Lys Leu Glu Thr Val Trp Leu Ser 785 790 795	2582
GGG ATT TGC CAG AAT GAG AAG AAC GAG GTG ATG AGC AGC AAG CTG GAC Gly Ile Cys Gln Asn Glu Lys Asn Glu Val Met Ser Ser Lys Leu Asp 800 805 810	2630
ATC GAC AAC ATG GGA GGC GTC TTC TAC ATG CTG CTG GTG GCC ATG GGG Ile Asp Asn Met Gly Val Phe Tyr Met Leu Leu Val Ala Met Gly 815 820 825 830	2678
CTG GCC CTG CTG GTC TTC GCC TGG GAG CAC CTG GTC TAC TGG AAG CTG Leu Ala Leu Val Phe Ala Trp Glu His Leu Val Tyr Trp Lys Leu 835 840 845	2726
CGC CAC TCG GTG CCC AAC TCA TCC CAG CTG GAC TTC CTG CTG GCT TTC Arg His Ser Val Pro Asn Ser Ser Gln Leu Asp Phe Leu Leu Ala Phe 850 855 860	2774
AGC AGG GGC ATC TAC AGC TGC TTC AGC GGG GTG CAG AGC CTC GCC AGC Ser Arg Gly Ile Tyr Ser Cys Phe Ser Gly Val Gln Ser Leu Ala Ser 865 870 875	2822
CCA CCG CGG CAG GCC AGC CCG GAC CTC ACG GCG AGC TCG GCC CAG GCC Pro Pro Arg Gln Ala Ser Pro Asp Leu Thr Ala Ser Ser Ala Gln Ala 880 885 890	2870
AGC GTG CTC AAG ATT CTG CAG GCA GCC CGC GAC ATG GTG ACC ACG GCG Ser Val Leu Lys Ile Leu Gln Ala Ala Arg Asp Met Val Thr Thr Ala 895 900 905 910	2918
GGC GTA AGC AAC TCC CTG GAC CGC GCC ACT CGC ACC ATC GAG AAT TGG Gly Val Ser Asn Ser Leu Asp Arg Ala Thr Arg Thr Ile Glu Asn Trp 915 920 925	2966
GGT GGC GGC CGC CGT GCG CCC CCA CCG TCC CCC TGC CCG ACC CCG CGG Gly Gly Gly Arg Arg Ala Pro Pro Pro Ser Pro Cys Pro Thr Pro Arg 930 935 940	3014

TCT GGC CCC AGC CCA TGC CTG CCC ACC CCC GAC CCG CCC CCA GAG CCG	3062
Ser Gly Pro Ser Pro Cys Leu Pro Thr Pro Asp Pro Pro Pro Glu Pro	
945 950 955	
AGC CCC ACG GGC TGG GGA CCG CCA GAC GGG GGT CGC GCG GCG CTT GTG	3110
Ser Pro Thr Gly Trp Gly Pro Pro Asp Gly Gly Arg Ala Ala Leu Val	
960 965 970	
CGC AGG GCT CCG CAG CCC CCG GGC CGC CCC CCG ACG CCG GGG CCG CCC	3158
Arg Arg Ala Pro Gln Pro Pro Gly Arg Pro Pro Thr Pro Gly Pro Pro	
975 980 985 990	
CTG TCC GAC GTC TCC CGA GTG TCG CGC CGC CCA GCC TGG GAG GCG CGG	3206
Leu Ser Asp Val Ser Arg Val Ser Arg Arg Pro Ala Trp Glu Ala Arg	
995 1000 1005	
TGG CCG GTG CGG ACC GGG CAC TGC GGG AGG CAC CTC TCG GCC TCC GAG	3254
Trp Pro Val Arg Thr Gly His Cys Gly Arg His Leu Ser Ala Ser Glu	
1010 1015 1020	
CGG CCC CTG TCG CCC GCG CGC TGT CAC TAC AGC TCC TTT CCT CGA GCC	3302
Arg Pro Leu Ser Pro Ala Arg Cys His Tyr Ser Ser Phe Pro Arg Ala	
1025 1030 1035	
GAC CGA TCC GGC CGC CCC TTC CTC CCG CTC TTC CCG GAG CCC CCG GAG	3350
Asp Arg Ser Gly Arg Pro Phe Leu Pro Leu Phe Pro Glu Pro Pro Glu	
1040 1045 1050	
CTG GAG GAC CTG CCG CTG CTC GGT CCG GAG CAG CTG GCC CGG CGG GAG	3398
Leu Glu Asp Leu Pro Leu Leu Gly Pro Glu Gln Leu Ala Arg Arg Glu	
1055 1060 1065 1070	
GCC CTG CTG AAC GCG GCC TGG GCC CGG GGC TCG CGC CCG AGT CAC GCT	3446
Ala Leu Leu Asn Ala Ala Trp Ala Arg Gly Ser Arg Pro Ser His Ala	
1075 1080 1085	
TCC CTG CCC AGC TCC GTG GCC GAG GCC TTC GCT CGG CCC AGC TCG CTG	3494
Ser Leu Pro Ser Ser Val Ala Glu Ala Phe Ala Arg Pro Ser Ser Leu	
1090 1095 1100	
CCC GCT GGG TGC ACC GGC CCC GCC TGC GCC CGC CCC GAC GGC CAC TCG	3542
Pro Ala Gly Cys Thr Gly Pro Ala Cys Ala Arg Pro Asp Gly His Ser	
1105 1110 1115	
GCC TGC AGG CGC TTG GCG CAG GCG CAG TCG ATG TGC TTG CCG ATC TAC	3590
Ala Cys Arg Arg Leu Ala Gln Ala Gln Ser Met Cys Leu Pro Ile Tyr	
1120 1125 1130	
CGG GAG GCC TGC CAG GAG GGC GAG CAG GCA GGG GCC CCC GCC TGG CAG	3638
Arg Glu Ala Cys Gln Glu Gly Glu Gln Ala Gly Ala Pro Ala Trp Gln	
1135 1140 1145 1150	
CAC AGA CAG CAC GTC TGC CTG CAC GCC CAC GGC CAC CTG CCA TTG TGC	3686
His Arg Gln His Val Cys Leu His Ala His Ala His Leu Pro Leu Cys	
1155 1160 1165	
TGG GGG GCT GTC TGT CCT CAC CTT CCA CCC TGT GAC AGC CAC GGC TCC	3734
Trp Gly Ala Val Cys Pro His Leu Pro Pro Cys Asp Ser His Gly Ser	
1170 1175 1180	
TGG CCT TCC GGC GCC TGG GGG CCT CTG GGG CAC AGC GGC AGG ACT CTG	3782
Trp Leu Ser Gly Ala Trp Gly Pro Leu Gly His Ser Gly Arg Thr Leu	
1185 1190 1195	
GGG CTG GGC ACA GGC TAC AGA GAC AGT GGG GGA CTG GAC GAG ATC AGC	3830
Gly Leu Gly Thr Gly Tyr Arg Asp Ser Gly Gly Leu Asp Glu Ile Ser	
1200 1205 1210	

AGT GTA GCC CGT CGG AGG CAA GGC TTC CCG GGA CCC TGC ACC TGG AGA	3878
Ser Val Ala Arg Glu Thr Gln Gly Phe Pro Gly Pro Cys Thr Trp Arg	
1215 1221 1225 1230	
CGG ATC TCC AGT CTG GAG TCA GAA GTG TGAGTTATCA GCCACTCAGG	3925
Arg Ile Ser Ser Leu Glu Ser Glu Val	
1235 124	
CTCCGAGCCA GCTGGATTCT CTGCCTGCCA CTGTCAGGGT TAAGCGGCAG GCAGGATTGG	3985
CCCTTCTCTG GCTTCTACCA TGAAATCCTG GCCATGGCAC CCCAGTGACA GATGATGTCT	4045
TCCATGGTCA TCAGTGACCT CAGCTAGCCT CA	4077

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1239 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Met Gly Gly Ala Leu Gly Pro Ala Leu Leu Leu Thr Ser Leu Phe Gly	
1 5 10 15	
Ala Trp Ala Gly Leu Gly Pro Gly Gln Gly Glu Gln Gly Met Thr Val	
20 25 30	
Ala Val Val Phe Ser Ser Ser Gly Pro Pro Gln Ala Gln Phe Arg Val	
35 40 45	
Arg Leu Thr Pro Gin Ser Phe Leu Asp Leu Pro Leu Glu Ile Gln Pro	
50 55 60	
Leu Thr Val Gly Val Asn Thr Thr Asn Pro Ser Ser Leu Leu Thr Gln	
65 70 75 80	
Ile Cys Gly Leu Leu Gly Ala Ala His Val His Gly Ile Val Phe Glu	
85 90 95	
Asp Asn Val Asp Thr Glu Ala Val Ala Gln Ile Leu Asp Phe Ile Ser	
100 105 110	
Ser Gln Thr His Val Pro Ile Leu Ser Ile Ser Gly Gly Ser Ala Val	
115 120 125	
Val Leu Thr Pro Lys Glu Pro Gly Ser Ala Phe Leu Gln Leu Gly Val	
130 135 140	
Ser Leu Glu Gln Gln Leu Gln Val Leu Phe Lys Val Leu Glu Glu Tyr	
145 150 155 160	
Asp Trp Ser Ala Phe Ala Val Ile Thr Ser Leu His Pro Gly His Ala	
165 170 175	
Leu Phe Leu Glu Gly Val Arg Ala Val Ala Asp Ala Ser His Val Ser	
180 185 190	
Trp Arg Leu Leu Asp Val Val Thr Leu Glu Leu Asp Pro Gly Gly Pro	
195 200 205	
Arg Ala Arg Thr Gln Arg Leu Leu Arg Gln Leu Asp Ala Pro Val Phe	
210 215 220	

Val Ala Tyr Cys Ser Arg Glu Glu Ala Glu Val Leu Phe Ala Glu Ala
225 230 235 240

Ala Gln Ala Gly Leu Val Gly Pro Gly His Val Trp Leu Val Pro Asn
245 250 255

Leu Ala Leu Gly Ser Thr Asp Ala Pro Pro Ala Thr Phe Pro Val Gly
260 265 270

Leu Ile Ser Val Val Thr Glu Ser Trp Arg Leu Ser Leu Arg Gln Lys
275 280 285

Val Arg Asp Gly Val Ala Ile Leu Ala Leu Gly Ala His Ser Tyr Trp
290 295 300

Arg Gln His Gly Thr Leu Pro Ala Pro Ala Gly Asp Cys Arg Val His
305 310 315 320

Pro Gly Pro Val Ser Pro Ala Arg Glu Ala Phe Tyr Arg His Leu Leu
325 330 335

Asn Val Thr Trp Glu Gly Arg Asp Phe Ser Phe Ser Pro Gly Gly Tyr
340 345 350

Leu Val Gln Pro Thr Met Val Val Ile Ala Leu Asn Arg His Arg Leu
355 360 365

Trp Glu Met Val Gly Arg Trp Glu His Gly Val Leu Tyr Met Lys Tyr
370 375 380

Pro Val Trp Pro Arg Tyr Ser Ala Ser Leu Gln Pro Val Val Asp Ser
385 390 395 400

Arg His Leu Thr Val Ala Thr Leu Glu Glu Arg Pro Phe Val Ile Val
405 410 415

Glu Ser Pro Asp Pro Gly Thr Gly Gly Cys Val Pro Asn Thr Val Pro
420 425 430

Cys Arg Arg Gln Ser Asn His Thr Phe Ser Ser Gly Asp Val Ala Pro
435 440 445

Tyr Thr Lys Leu Cys Cys Lys Gly Phe Cys Ile Asp Ile Leu Lys Lys
450 455 460

Leu Ala Arg Val Val Lys Phe Ser Tyr Asp Leu Tyr Leu Val Thr Asn
465 470 475 480

Gly Lys His Gly Lys Arg Val Arg Gly Val Trp Asn Gly Met Ile Gly
485 490 495

Glu Val Tyr Tyr Lys Arg Ala Asp Met Ala Ile Gly Ser Leu Thr Ile
500 505 510

Asn Glu Glu Arg Ser Glu Ile Val Asp Phe Ser Val Pro Phe Val Glu
515 520 525

Thr Gly Ile Ser Val Met Val Ala Arg Ser Asn Gly Thr Val Ser Pro
530 535 540

Ser Ala Phe Leu Glu Pro Tyr Ser Pro Ala Val Trp Val Met Met Phe
545 550 555 560

Val Met Cys Leu Thr Val Val Ala Ile Thr Val Phe Met Phe Glu Tyr
565 570 575

Phe Ser Pro Val Ser Tyr Asn Gln Asn Leu Thr Arg Gly Lys Thr Phe
580 585 590

Thr Ile Gly Lys Ser Val Trp Leu Leu Trp Ala Leu Val Phe Asn Asn
595 600 605

Ser Val Pro Ile Glu Asn Pro Arg Gly Thr Thr Ser Lys Ile Met Val
610 615 620

Leu Val Trp Ala Phe Phe Ala Val Ile Phe Leu Ala Arg Tyr Thr Ala
625 630 635 640

Asn Leu Ala Ala Phe Met Ile Gln Glu Gln Tyr Ile Asp Thr Val Ser
645 650 655

Gly Leu Ser Asp Lys Lys Phe Gln Arg Pro Gln Asp Gln Tyr Pro Pro
660 665 670

Phe Arg Phe Gly Thr Val Pro Asn Gly Ser Thr Glu Arg Asn Ile Arg
675 680 685

Ser Asn Tyr Arg Asp Met His Thr His Met Val Lys Phe Asn Gln Arg
690 695 700

Ser Val Glu Asp Ala Leu Thr Ser Leu Lys Met Gly Ser Glu Ala Gln
705 710 715 720

Pro Val Pro Arg Lys Leu Asp Ala Phe Ile Tyr Asp Ala Ala Val Leu
725 730 735

Asn Tyr Met Ala Gly Lys Asp Glu Gly Cys Lys Leu Val Thr Ile Gly
740 745 750

Ser Gly Lys Val Phe Ala Thr Thr Gly Tyr Gly Ile Ala Met Gln Lys
755 760 765

Asp Ser His Trp Lys Arg Ala Ile Asp Leu Ala Leu Leu Gln Phe Leu
770 775 780

Gly Asp Gly Glu Thr Gln Lys Leu Glu Thr Val Trp Leu Ser Gly Ile
785 790 795 800

Cys Gln Asn Glu Lys Asn Glu Val Met Ser Ser Lys Leu Asp Ile Asp
805 810 815

Asn Met Gly Val Phe Tyr Met Leu Leu Val Ala Met Gly Leu Ala
820 825 830

Leu Leu Val Phe Ala Trp Glu His Leu Val Tyr Trp Lys Leu Arg His
835 840 845

Ser Val Pro Asn Ser Ser Gln Leu Asp Phe Leu Leu Ala Phe Ser Arg
850 855 860

Gly Ile Tyr Ser Cys Phe Ser Gly Val Gln Ser Leu Ala Ser Pro Pro
865 870 875 880

Arg Gln Ala Ser Pro Asp Leu Thr Ala Ser Ser Ala Gln Ala Ser Val
885 890 895

Leu Lys Ile Leu Gln Ala Ala Arg Asp Met Val Thr Thr Ala Gly Val
900 905 910

Ser Asn Ser Leu Asp Arg Ala Thr Arg Thr Ile Glu Asn Trp Gly Gly
915 920 925

Gly Arg Arg Ala Pro Pro Pro Ser Pro Cys Pro Thr Pro Arg Ser Gly
930 935 940

Pro Ser Pro Cys Leu Pro Thr Pro Asp Pro Pro Pro Glu Pro Ser Pro
945 950 955 960

Thr Gly Trp Gly Pro Pro Asp Gly Gly Arg Ala Ala Leu Val Arg Arg
965 970 975

Ala Pro Gln Pro Pro Gly Arg Pro Pro Thr Pro Gly Pro Pro Leu Ser
980 985 990

Asp Val Ser Arg Val Ser Arg Arg Pro Ala Trp Glu Ala Arg Trp Pro
995 1000 1005

Val Arg Thr Gly His Cys Gly Arg His Leu Ser Ala Ser Glu Arg Pro
1010 1015 1020

Leu Ser Pro Ala Arg Cys His Tyr Ser Ser Phe Pro Arg Ala Asp Arg
1025 1030 1035 1040

Ser Gly Arg Pro Phe Leu Pro Leu Phe Pro Glu Pro Pro Glu Leu Glu
1045 1050 1055

Asp Leu Pro Leu Leu Gly Pro Glu Gln Leu Ala Arg Arg Glu Ala Leu
1060 1065 1070

Leu Asn Ala Ala Trp Ala Arg Gly Ser Arg Pro Ser His Ala Ser Leu
1075 1080 1085

Pro Ser Ser Val Ala Glu Ala Phe Ala Arg Pro Ser Ser Leu Pro Ala
1090 1095 1100

Gly Cys Thr Gly Pro Ala Cys Ala Arg Pro Asp Gly His Ser Ala Cys
1105 1110 1115 1120

Arg Arg Leu Ala Gln Ala Gln Ser Met Cys Leu Pro Ile Tyr Arg Glu
1125 1130 1135

Ala Cys Gln Glu Gly Glu Gln Ala Gly Ala Pro Ala Trp Gln His Arg
1140 1145 1150

Gln His Val Cys Leu His Ala His Ala His Leu Pro Leu Cys Trp Gly
1155 1160 1165

Ala Val Cys Pro His Leu Pro Pro Cys Asp Ser His Gly Ser Trp Leu
1170 1175 1180

Ser Gly Ala Trp Gly Pro Leu Gly His Ser Gly Arg Thr Leu Gly Leu
1185 1190 1195 1200

Gly Thr Gly Tyr Arg Asp Ser Gly Gly Leu Asp Glu Ile Ser Ser Val
1205 1210 1215

Ala Arg Gly Thr Gln Gly Phe Pro Gly Pro Cys Thr Trp Arg Arg Ile
1220 1225 1230

Ser Ser Leu Glu Ser Glu Val
1235

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4002 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: both
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 189..3833

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

CCCTTAATAA GATTTGCNAC GTACACTCGA GCCATCGCGA GTGTCCTTGA	60
ACGGTGGCTC TCGCTGCTCG CGCCCCCTCC TCCCAGGGGG GGAGCCTGAT	120
CTATGAATTAA TTTATGCCCG GCCTAAAAAT ACCCCGAACT TCACAGCCCG	180
CGGTGGAC ATG GGT GGG GCC CTG GGG CCG GCC CTG TTG CTC ACC	230
Met Gly Gly Ala Leu Gly Pro Ala Leu Leu Thr Ser Leu	
1 5 10	
TTC GGT GCC TGG GCA GGG CTG GGT CCG GGG CAG GGC GAG CAG	278
Phe Gly Ala Trp Ala Gly Leu Gly Pro Gly Gln Gly Glu Gln Gly Met	
15 20 25 30	
ACG GTG GCC GTG GTG TTT AGC AGC TCA GGG CCG CCC CAG GCC CAG	326
Thr Val Ala Val Val Phe Ser Ser Ser Gly Pro Pro Gln Ala Gln Phe	
35 40 45	
CGT GTC CGC CTC ACC CCC CAG AGC TTC CTG GAC CTA CCC CTG GAG	374
Arg Val Arg Leu Thr Pro Gln Ser Phe Leu Asp Leu Pro Leu Glu Ile	
50 55 60	
CAG CCG CTC ACA GTT GGG GTC AAC ACC ACC AAC CCC AGC AGC CTC CTC	422
Gln Pro Leu Thr Val Gly Val Asn Thr Thr Asn Pro Ser Ser Leu Leu	
65 70 75	
ACC CAG ATC TGC GGC CTC CTG GGT GCT GCC CAC GTC CAC GGC ATT GTC	470
Thr Gln Ile Cys Gly Leu Leu Gly Ala Ala His Val His Gly Ile Val	
80 85 90	
TTT GAG GAC AAC GTG GAC ACC GAG GCG GTG GCC CAG ATC CTT GAC TTC	518
Phe Glu Asp Asn Val Asp Thr Glu Ala Val Ala Gln Ile Leu Asp Phe	
95 100 105 110	
ATC TCC TCC CAG ACC CAT GTG CCC ATC CTC AGC ATC AGC GGA GGC TCT	566
Ile Ser Ser Gln Thr His Val Pro Ile Leu Ser Ile Ser Gly Gly Ser	
115 120 125	
GCT GTG GTC CTC ACC CCC AAG GAG CCG GGC TCC GCC TTC CTG CAG CTG	614
Ala Val Val Leu Thr Pro Lys Glu Pro Gly Ser Ala Phe Leu Gln Leu	
130 135 140	
GGC GTG TCC CTG GAG CAG CAG CTG CAG GTG CTG TTC AAG GTG CTG GAA	662
Gly Val Ser Leu Glu Gln Gln Leu Gln Val Leu Phe Lys Val Leu Glu	
145 150 155	
GAG TAC GAC TGG AGC GCC TTC GCC GTC ATC ACC AGC CTG CAC CCG GGC	710
Glu Tyr Asp Trp Ser Ala Phe Ala Val Ile Thr Ser Leu His Pro Gly	
160 165 170	
CAC GCG CTC TTC CTG GAG GGC GTG CGC GCC GTC GCC GAC GCC AGC CAC	758
His Ala Leu Phe Leu Glu Gly Val Arg Ala Val Ala Asp Ala Ser His	
175 180 185 190	

GTG AGT TGG CGG CTG CTG GAC GTG GTG AGC ATG GAA CTG GAC CCG GGA Val Ser Trp Arg Leu Leu Asp Val Val Thr Leu Glu Leu Asp Pro Gly 195 200 205	806
GCG CGC CGC GCG CGC ACG CAG CGC CTG CTG CGC CAG CTC GAC GCG CCC Gly Pro Arg Ala Arg Thr Gln Arg Leu Leu Arg Gln Leu Asp Ala Pro 210 215 220	854
GTG TTT GTG GCC TAC TGC TCG CGC GAG GAG GCC GAG GTG CTC TTC GCC Val Phe Val Ala Tyr Cys Ser Arg Glu Glu Ala Glu Val Leu Phe Ala 225 230 235	902
GAG GCG GCG CAG GCC GGT CTG GTG GGG CCC GGC CAC GTG TGG CTG GTG Glu Ala Ala Gln Ala Gly Leu Val Gly Pro Gly His Val Trp Leu Val 240 245 250	950
CCC AAC CTG GCG CTG GGC AGC ACC GAT GCG CCC CCC GCC ACC TTC CCC Pro Asn Leu Ala Leu Gly Ser Thr Asp Ala Pro Pro Ala Thr Phe Pro 255 260 265 270	998
GTG GGC CTC ATC AGC GTC GTC ACC GAG AGC TGG CGC CTC AGC CTG CGC Val Gly Leu Ile Ser Val Val Thr Glu Ser Trp Arg Leu Ser Leu Arg 275 280 285	1046
CAG AAG GTG CGC GAC GGC GTG GCC ATT CTG GCC CTG GGC GCC CAC AGC Gln Lys Val Arg Asp Gly Val Ala Ile Leu Ala Leu Gly Ala His Ser 290 295 300	1094
TAC TGG CGC CAG CAT GGA ACC CTG CCA GCC CCG GCC GGG GAC TGC CGT Tyr Trp Arg Gln His Gly Thr Leu Pro Ala Pro Ala Gly Asp Cys Arg 305 310 315	1142
GTT CAC CCT GGG CCC GTC AGC CCT GCC CGG GAG GCC TTC TAC AGG CAC Val His Pro Gly Pro Val Ser Pro Ala Arg Glu Ala Phe Tyr Arg His 320 325 330	1190
CTA CTG AAT GTC ACC TGG GAG GGC CGA GAC TTC TCC TTC AGC CCT GGT Leu Leu Asn Val Thr Trp Glu Gly Arg Asp Phe Ser Phe Ser Pro Gly 335 340 345 350	1238
GGG TAC CTG GTC CAG CCC ACC ATG GTG GTG ATC GCC CTC AAC CGG CAC Gly Tyr Leu Val Gln Pro Thr Met Val Val Ile Ala Leu Asn Arg His 355 360 365	1286
CGC CTC TGG GAG ATG GTG GGG CGC TGG GAG CAT GGC GTC CTA TAC ATG Arg Leu Trp Glu Met Val Gly Arg Trp Glu His Gly Val Leu Tyr Met 370 375 380	1334
AAG TAC CCC GTG TGG CCT CGC TAC AGT GGC TCT CTG CAG CCT GTG GTG Lys Tyr Pro Val Trp Pro Arg Tyr Ser Ala Ser Leu Gln Pro Val Val 385 390 395	1382
GAC AGT CGG CAC CTG ACG GTG GCC ACG CTG GAA GAG CGG CCC TTT GTC Asp Ser Arg His Leu Thr Val Ala Thr Leu Glu Glu Arg Pro Phe Val 400 405 410	1430
ATC GTG GAG AGC CCT GAC CCT GGC ACA GGA GGC TGT GTC CCC AAC ACC Ile Val Glu Ser Pro Asp Pro Gly Thr Gly Gly Cys Val Pro Asn Thr 415 420 425 430	1478
GTC CCC TGC CGC AGG CAG AGC AAC CAC ACC TTC AGC AGC GGG GAC GTG Val Pro Cys Arg Arg Gln Ser Asn His Thr Phe Ser Ser Gly Asp Val 435 440 445	1526
GCC CCC TAC ACC AAG CTC TGC TGT AAG GGA TTC TGC ATC GAC ATC CTC Ala Pro Tyr Thr Lys Leu Cys Cys Lys Gly Phe Cys Ile Asp Ile Leu 450 455 460	1574

AAG AAG CTG GCC AGA GTG GTC AAA TTC TCC TAC GAC CTG TAC CTG GTG Lys Lys Leu Ala Arg Val Val Lys Phe Ser Tyr Asp Leu Tyr Leu Val 465 470 475	1622
ACC AAC GGC AAG CAT GGC AAG CGG GTG CGC GGC GTA TGG AAC GGC ATG Thr Asn Gly Lys His Gly Lys Arg Val Arg Gly Val Trp Asn Gly Met 480 485 490	1670
ATT GGG GAG GTG TAC TAC AAG CGG GCA GAC ATG GCC ATC GGC TCC CTC Ile Gly Glu Val Tyr Tyr Lys Arg Ala Asp Met Ala Ile Gly Ser Leu 495 500 505 510	1718
ACC ATC AAT GAG GAA CGC TCC GAG ATC GTA GAC TTC TCT GTA CCC TTT Thr Ile Asn Glu Glu Arg Ser Glu Ile Val Asp Phe Ser Val Pro Phe 515 520 525	1766
GTG GAG ACG GGC ATC AGT GTG ATG GTG GCT CGC AGC AAT GGC ACC GTC Val Glu Thr Gly Ile Ser Val Met Val Ala Arg Ser Asn Gly Thr Val 530 535 540	1814
TCC CCC TCG GCC TTC TTG GAG CCA TAT AGC CCT GCA GTG TGG GTG ATG Ser Pro Ala Phe Leu Glu Pro Tyr Ser Pro Ala Val Trp Val Met 545 550 555	1862
ATG TTT GTC ATG TGC CTC ACT GTG GTG GCC ATC ACC GTC TTC ATG TTC Met Phe Val Met Cys Leu Thr Val Val Ala Ile Thr Val Phe Met Phe 560 565 570	1910
GAG TAC TTC AGC CCT GTC AGC TAC AAC CAG AAC CTC ACC AGA GGC AAG Glu Tyr Phe Ser Pro Val Ser Tyr Asn Gln Asn Leu Thr Arg Gly Lys 575 580 585 590	1958
ACT TTC ACT ATC GGC AAG TCC GTG TGG CTG CTG TGG GCG CTG GTC TTC Thr Phe Thr Ile Gly Lys Ser Val Trp Leu Leu Trp Ala Leu Val Phe 595 600 605	2006
AAC AAC TCA GTG CCC ATC GAG AAC CCG CGG GGC ACC ACC AGC AAG ATC Asn Asn Ser Val Pro Ile Glu Asn Pro Arg Gly Thr Thr Ser Lys Ile 610 615 620	2054
ATG GTT CTG GTC TGG GCC TTC TTT GCT GTC ATC TTC CTC GCC AGA TAC Met Val Leu Val Trp Ala Phe Phe Ala Val Ile Phe Leu Ala Arg Tyr 625 630 635	2102
ACG GCC AAC CTG GCC TTC ATG ATC CAA GAG CAA TAC ATC GAC ACT Thr Ala Asn Leu Ala Phe Met Ile Gln Glu Gln Tyr Ile Asp Thr 640 645 650	2150
GTG TCG GGC CTC AGT GAC AAG AAG TTT CAG CGG CCT CAA GAT CAG TAC Val Ser Gly Leu Ser Asp Lys Lys Phe Gln Arg Pro Gln Asp Gln Tyr 655 660 665 670	2198
CCA CCT TTC CGC TTC GGC ACG GTG CCC AAC GGC AGC ACG GAG CGG AAC Pro Pro Phe Arg Phe Gly Thr Val Pro Asn Gly Ser Thr Glu Arg Asn 675 680 685	2246
ATC CGC AGT AAC TAC CGT GAC ATG CAC ACC CAC ATG GTC AAG TTC AAC Ile Arg Ser Asn Tyr Arg Asp Met His Thr His Met Val Lys Phe Asn 690 695 700	2294
CAG CGC TCG GTG GAG GAC GCG CTC ACC AGC CTC AAG ATG GGC AAG GAC Gln Arg Ser Val Glu Asp Ala Leu Thr Ser Leu Lys Met Gly Lys Asp 705 710 715	2342
GAG GGC TGC AAG CTG GTC ACC ATT GGG TCT GGC AAG GTC TTT GCT ACC Glu Gly Cys Lys Leu Val Thr Ile Gly Ser Gly Lys Val Phe Ala Thr 720 725 730	2390

ACT GGC TAC GGC ATC GCC ATG CAG AAG GAC TCC CAC TGG AAG CGG GCC Thr Gly Tyr Gly Ile Ala Met Gln Lys Asp Ser His Trp Lys Arg Ala 735 740 745 750	2438
ATA GAC CTG GCG CTC TTG CAG TTC CTG GGG GAC GGA GAG ACA CAG AAA Ile Asp Leu Ala Leu Gln Phe Leu Gly Asp Gly Glu Thr Gln Lys 755 760 765	2486
CTG GAG ACA GTG TGG CTC TCA GGG ATC TGC CAG AAT GAG AAG AAC GAG Leu Glu Thr Val Trp Leu Ser Gly Ile Cys Gln Asn Glu Lys Asn Glu 770 775 780	2534
G TG ATG AGC AGC AAG CTG GAC ATC GAC AAC ATG GGA GGC GTC TTC TAC Val Met Ser Ser Lys Leu Asp Ile Asp Asn Met Gly Gly Val Phe Tyr 785 790 795	2582
ATG CTG CTG GTG GCC ATG GG3 CTG GCC CTG CTG GTC TTC GCC TGG GAG Met Leu Leu Val Ala Met Gly Leu Ala Leu Leu Phe Ala Trp Glu 800 805 810	2630
CAC CTG GTC TAC TGG AAG CTG CGC CAC TCG GTG CCC AAC TCA TCC CAG His Leu Val Tyr Trp Lys Leu Arg His Ser Val Pro Asn Ser Ser Gln 815 820 825 830	2678
CTG GAC TTC CTG CTG GCT TTC AGC AGG GGC ATC TAC AGC TGC TTC AGC Leu Asp Phe Leu Leu Ala Phe Ser Arg Gly Ile Tyr Ser Cys Phe Ser 835 840 845	2726
GGG GTG CAG AGC CTC GCC AGC CCA CCG CGG CAG GCC AGC CCG GAC CTC Gly Val Gln Ser Leu Ala Ser Pro Pro Arg Gln Ala Ser Pro Asp Leu 850 855 860	2774
ACG GCC AGC TCG GCC CAG GCC AGC GTG CTC AAG ATT CTG CAG GCA GCC Thr Ala Ser Ser Ala Gln Ala Ser Val Leu Lys Ile Leu Gln Ala Ala 865 870 875	2822
CGC GAC ATG GTG ACC ACG GCG GGC GTA AGC AAC TCC CTG GAC CGC GCC Arg Asp Met Val Thr Thr Ala Gly Val Ser Asn Ser Leu Asp Arg Ala 880 885 890	2870
ACT CGC ACC ATC GAG AAT TGG GGT GGC GGC CGC CGT GCG CCC CCA CCG Thr Arg Thr Ile Glu Asn Trp Gly Gly Arg Arg Ala Pro Pro Pro 895 900 905 910	2918
TCC CCC TGC CCG ACC CCG CGG TCT GGC CCC AGC CCA TGC CTG CCC ACC Ser Pro Cys Pro Thr Pro Arg Ser Gly Pro Ser Pro Cys Leu Pro Thr 915 920 925	2966
CCC GAC CCG CCC CCA GAG CCG AGC CCC ACG GGC TGG GGA CCG CCA GAC Pro Asp Pro Pro Pro Glu Pro Ser Pro Thr Gly Trp Gly Pro Pro Asp 930 935 940	3014
GGG GGT CGC GCG GCG CTT GTG CGC AGG GCT CCG CAG CCC CCG GGC CGC Gly Gly Arg Ala Ala Leu Val Arg Arg Ala Pro Gln Pro Pro Gly Arg 945 950 955	3062
CCC CCG ACG CCG GGG CCG CCC CTG TCC GAC GTC TCC CGA GTG TCG CGC Pro Pro Thr Pro Gly Pro Pro Leu Ser Asp Val Ser Arg Val Ser Arg 960 965 970	3110
CGC CCA GCC TGG GAG GCG CGG TGG CCG GTG CGG ACC GGG CAC TGC GGG Arg Pro Ala Trp Glu Ala Arg Trp Pro Val Arg Thr Gly His Cys Gly 975 980 985 990	3158
AGG CAC CTC TCG GCC TCC GAG CGG CCC CTG TCG CCC GCG CGC TGT CAC Arg His Leu Ser Ala Ser Glu Arg Pro Leu Ser Pro Ala Arg Cys His 995 1000 1005	3206

TAC AGC TCC TTT CCT CGA GCC CGA CGA TCC GGC CGC CCC TTC CTC CCG Tyr Ser Ser Phe Pro Arg Ala Asp Arg Ser Gly Arg Pro Phe Leu Pro 1010 1015 1020	3254
CTC TTC CCG GAG CCC CCG GAG CTG GAG GAC CTG CCG CTG CTC GGT CCG Leu Phe Pro Glu Pro Pro Glu Leu Glu Asp Leu Pro Leu Leu Gly Pro 1025 1030 1035	3302
GAG CAG CTG GCC CGG CGG GAG GCC CTG CTG AAC GCG GCC TGG GCC CGG Glu Gln Leu Ala Arg Arg Glu Ala Leu Leu Asn Ala Ala Trp Ala Arg 1040 1045 1050	3350
GGC TCG CGC CCG AGT CAC GCT TCC CTG CCC AGC TCC GTG GCC GAG GCC Gly Ser Arg Pro Ser His Ala Ser Leu Pro Ser Ser Val Ala Glu Ala 1055 1060 1065 1070	3398
TTC GCT CGG CCC AGC TCG CTG CCC GCT GGG TGC ACC GGC CCC GCC TGC Phe Ala Arg Pro Ser Ser Leu Pro Ala Gly Cys Thr Gly Pro Ala Cys 1075 1080 1085	3446
GCC CGC CCC GAC GGC CAC TCG GCC TGC AGG CGC TTG GCG CAG GCG CAG Ala Arg Pro Asp Gly His Ser Ala Cys Arg Arg Leu Ala Gln Ala Gln 1090 1095 1100	3494
TCG ATG TGC TTG CCG ATC TAC CGG GAG GCC TGC CAG GAG GGC GAG CAG Ser Met Cys Leu Pro Ile Tyr Arg Glu Ala Cys Gln Glu Gly Glu Gln 1105 1110 1115	3542
GCA GGG GCC CCC GCC TGG CAG CAC AGA CAG CAC GTC TGC CTG CAC GCC Ala Gly Ala Pro Ala Trp Gln His Arg Gln His Val Cys Leu His Ala 1120 1125 1130	3590
CAC GCC CAC CTG CCA TTG TGC TGG GGG GCT GTC TGT CCT CAC CTT CCA His Ala His Leu Pro Leu Cys Trp Gly Ala Val Cys Pro His Leu Pro 1135 1140 1145 1150	3638
CCC TGT GAC AGC CAC GGC TCC TGG CTC TCC GGC GCC TGG GGG CCT CTG Pro Cys Asp Ser His Gly Ser Trp Leu Ser Gly Ala Trp Gly Pro Leu 1155 1160 1165	3686
GGG CAC AGC GGC AGG ACT CTG GGG CTG GGC ACA GGC TAC AGA GAC AGT Gly His Ser Gly Arg Thr Leu Gly Leu Gly Thr Gly Tyr Arg Asp Ser 1170 1175 1180	3734
GGG GGA CTG GAC GAG ATC AGC AGT GTA GCC CGT GGG ACG CAA GGC TTC Gly Gly Leu Asp Glu Ile Ser Ser Val Ala Arg Gly Thr Gln Gly Phe 1185 1190 1195	3782
CCG GGA CCC TGC ACC TGG AGA CGG ATC TCC AGT CTG GAG TCA GAA GTG Pro Gly Pro Cys Thr Trp Arg Arg Ile Ser Ser Leu Glu Ser Glu Val 1200 1205 1210	3830
TGAGTTATCA GCCACTCAGG CTCCGAGCCA GCTGGATTCT CTGCCTGCCA CTGTCAGGGT	3890
TAAGCGGCAG GCAGGATTGG CCCTTCTCTG GCTTCTACCA TGAAATCCTG GCCATGGCAC	3950
CCCAGTGACA GATGATGTCT TCCATGGTCA TCAGTGACCT CAGCTAGCCT CA	4002

(2) INFORMATION FOR SEQ ID NO:54:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1214 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

Met Gly Gly Ala Leu Gly Pro Ala Leu Leu Leu Thr Ser Leu Phe Gly
1 5 10 15

Ala Trp Ala Gly Leu Gly Pro Gly Gln Gly Glu Gln Gly Met Thr Val
20 25 30

Ala Val Val Phe Ser Ser Ser Gly Pro Pro Gln Ala Gln Phe Arg Val
35 40 45

Arg Leu Thr Pro Gln Ser Phe Leu Asp Leu Pro Leu Glu Ile Gln Pro
50 55 60

Leu Thr Val Gly Val Asn Thr Thr Asn Pro Ser Ser Leu Leu Thr Gln
65 70 75 80

Ile Cys Gly Leu Leu Gly Ala Ala His Val His Gly Ile Val Phe Glu
85 90 95

Asp Asn Val Asp Thr Glu Ala Val Ala Gln Ile Leu Asp Phe Ile Ser
100 105 110

Ser Gln Thr His Val Pro Ile Leu Ser Ile Ser Gly Gly Ser Ala Val
115 120 125

Val Leu Thr Pro Lys Glu Pro Gly Ser Ala Phe Leu Gln Leu Gly Val
130 135 140

Ser Leu Glu Gln Gln Leu Gln Val Leu Phe Lys Val Leu Glu Glu Tyr
145 150 155 160

Asp Trp Ser Ala Phe Ala Val Ile Thr Ser Leu His Pro Gly His Ala
165 170 175

Leu Phe Leu Glu Gly Val Arg Ala Val Ala Asp Ala Ser His Val Ser
180 185 190

Trp Arg Leu Leu Asp Val Val Thr Leu Glu Leu Asp Pro Gly Gly Pro
195 200 205

Arg Ala Arg Thr Gln Arg Leu Leu Arg Gln Leu Asp Ala Pro Val Phe
210 215 220

Val Ala Tyr Cys Ser Arg Glu Glu Ala Glu Val Leu Phe Ala Glu Ala
225 230 235 240

Ala Gln Ala Gly Leu Val Gly Pro Gly His Val Trp Leu Val Pro Asn
245 250 255

Leu Ala Leu Gly Ser Thr Asp Ala Pro Pro Ala Thr Phe Pro Val Gly
260 265 270

Leu Ile Ser Val Val Thr Glu Ser Trp Arg Leu Ser Leu Arg Gln Lys
275 280 285

Val Arg Asp Gly Val Ala Ile Leu Ala Leu Gly Ala His Ser Tyr Trp
290 295 300

Arg Gln His Gly Thr Leu Pro Ala Pro Ala Gly Asp Cys Arg Val His
305 310 315 320

Pro Gly Pro Val Ser Pro Ala Arg Glu Ala Phe Tyr Arg His Leu Leu
325 330 335

Asn Val Thr Trp Glu Gly Arg Asp Phe Ser Phe Ser Pro Gly Gly Tyr
340 345 350

Leu Val Gln Pro Thr Met Val Val Ile Ala Leu Asn Arg His Arg Leu
355 360 365

Trp Glu Met Val Gly Arg Trp Glu His Gly Val Leu Tyr Met Lys Tyr
370 375 380

Pro Val Trp Pro Arg Tyr Ser Ala Ser Leu Gln Pro Val Val Asp Ser
385 390 395 400

Arg His Leu Thr Val Ala Thr Leu Glu Glu Arg Pro Phe Val Ile Val
405 410 415

Glu Ser Pro Asp Pro Gly Thr Gly Cys Val Pro Asn Thr Val Pro
420 425 430

Cys Arg Arg Gln Ser Asn His Thr Phe Ser Ser Gly Asp Val Ala Pro
435 440 445

Tyr Thr Lys Leu Cys Cys Lys Gly Phe Cys Ile Asp Ile Leu Lys Lys
450 455 460

Leu Ala Arg Val Val Lys Phe Ser Tyr Asp Leu Tyr Leu Val Thr Asn
465 470 475 480

Gly Lys His Gly Lys Arg Val Arg Gly Val Trp Asn Gly Met Ile Gly
485 490 495

Glu Val Tyr Tyr Lys Arg Ala Asp Met Ala Ile Gly Ser Leu Thr Ile
500 505 510

Asn Glu Glu Arg Ser Glu Ile Val Asp Phe Ser Val Pro Phe Val Glu
515 520 525

Thr Gly Ile Ser Val Met Val Ala Arg Ser Asn Gly Thr Val Ser Pro
530 535 540

Ser Ala Phe Leu Glu Pro Tyr Ser Pro Ala Val Trp Val Met Met Phe
545 550 555 560

Val Met Cys Leu Thr Val Val Ala Ile Thr Val Phe Met Phe Glu Tyr
565 570 575

Phe Ser Pro Val Ser Tyr Asn Gln Asn Leu Thr Arg Gly Lys Thr Phe
580 585 590

Thr Ile Gly Lys Ser Val Trp Leu Leu Trp Ala Leu Val Phe Asn Asn
595 600 605

Ser Val Pro Ile Glu Asn Pro Arg Gly Thr Thr Ser Lys Ile Met Val
610 615 620

Leu Val Trp Ala Phe Phe Ala Val Ile Phe Leu Ala Arg Tyr Thr Ala
625 630 635 640

Asn Leu Ala Ala Phe Met Ile Gln Glu Gln Tyr Ile Asp Thr Val Ser
645 650 655

Gly Leu Ser Asp Lys Lys Phe Gln Arg Pro Gln Asp Gln Tyr Pro Pro
660 665 670

Phe Arg Phe Gly Thr Val Pro Asn Gly Ser Thr Glu Arg Asn Ile Arg
675 680 685

Ser Asn Tyr Arg Asp Met His Thr His Met Val Lys Phe Asn Gln Arg
690 695 700

Ser Val Glu Asp Ala Leu Thr Ser Leu Lys Met Gly Lys Asp Glu Gly
705 710 715 720

Cys Lys Leu Val Thr Ile Gly Ser Gly Lys Val Phe Ala Thr Thr Gly
725 730 735

Tyr Gly Ile Ala Met Gln Lys Asp Ser His Trp Lys Arg Ala Ile Asp
740 745 750

Leu Ala Leu Leu Gln Phe Leu Gly Asp Gly Glu Thr Gln Lys Leu Glu
755 760 765

Thr Val Trp Leu Ser Gly Ile Cys Gln Asn Glu Lys Asn Glu Val Met
770 775 780

Ser Ser Lys Leu Asp Ile Asp Asn Met Gly Gly Val Phe Tyr Met Leu
785 790 795 800

Leu Val Ala Met Gly Leu Ala Leu Leu Val Phe Ala Trp Glu His Leu
805 810 815

Val Tyr Trp Lys Leu Arg His Ser Val Pro Asn Ser Ser Gln Leu Asp
820 825 830

Phe Leu Leu Ala Phe Ser Arg Gly Ile Tyr Ser Cys Phe Ser Gly Val
835 840 845

Gln Ser Leu Ala Ser Pro Pro Arg Gln Ala Ser Pro Asp Leu Thr Ala
850 855 860

Ser Ser Ala Gln Ala Ser Val Leu Lys Ile Leu Gln Ala Ala Arg Asp
865 870 875 880

Met Val Thr Thr Ala Gly Val Ser Asn Ser Leu Asp Arg Ala Thr Arg
885 890 895

Thr Ile Glu Asn Trp Gly Gly Arg Arg Ala Pro Pro Pro Ser Pro
900 905 910

Cys Pro Thr Pro Arg Ser Gly Pro Ser Pro Cys Leu Pro Thr Pro Asp
915 920 925

Pro Pro Pro Glu Pro Ser Pro Thr Gly Trp Gly Pro Pro Asp Gly Gly
930 935 940

Arg Ala Ala Leu Val Arg Arg Ala Pro Gln Pro Pro Gly Arg Pro Pro
945 950 955 960

Thr Pro Gly Pro Pro Leu Ser Asp Val Ser Arg Val Ser Arg Arg Pro
965 970 975

Ala Trp Glu Ala Arg Trp Pro Val Arg Thr Gly His Cys Gly Arg His
980 985 990

Leu Ser Ala Ser Glu Arg Pro Leu Ser Pro Ala Arg Cys His Tyr Ser
995 1000 1005

Ser Phe Pro Arg Ala Asp Arg Ser Gly Arg Pro Phe Leu Pro Leu Phe
1010 1015 1020

Pro Glu Pro Pro Glu Leu Glu Asp Leu Pro Leu Leu Gly Pro Glu Gln
1025 1030 1035 1040

Leu Ala Arg Arg Glu Ala Leu Leu Asn Ala Ala Trp Ala Arg Gly Ser
1045 1050 1055

Arg Pro Ser His Ala Ser Leu Pro Ser Ser Val Ala Glu Ala Phe Ala
1060 1065 1070

Arg Pro Ser Ser Leu Pro Ala Gly Cys Thr Gly Pro Ala Cys Ala Arg
1075 1080 1085

Pro Asp Gly His Ser Ala Cys Arg Arg Leu Ala Gln Ala Gln Ser Met
1090 1095 1100

Cys Leu Pro Ile Tyr Arg Glu Ala Cys Gln Glu Gly Glu Gln Ala Gly
1105 1110 1115 1120

Ala Pro Ala Trp Gln His Arg Gln His Val Cys Leu His Ala His Ala
1125 1130 1135

His Leu Pro Leu Cys Trp Gly Ala Val Cys Pro His Leu Pro Pro Cys
1140 1145 1150

Asp Ser His Gly Ser Trp Leu Ser Gly Ala Trp Gly Pro Leu Gly His
1155 1160 1165

Ser Gly Arg Thr Leu Gly Leu Gly Thr Gly Tyr Arg Asp Ser Gly Gly
1170 1175 1180

Leu Asp Glu Ile Ser Ser Val Ala Arg Gly Thr Gln Gly Phe Pro Gly
1185 1190 1195 1200

Pro Cys Thr Trp Arg Arg Ile Ser Ser Leu Glu Ser Glu Val
1205 1210

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5538 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 210..4664

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

TTGAATTTGC ATCTCTTCAA GACACAAGAT TAAAACAAAA TTTACGCTAA ATTGGATTTC 60
AAATTATCTT CCGTTCATTT ATCCTTCGTC TTTCTTATGT GGATATGCAA GCGAGAAGAA 120
GGGACTGGAC ATTCCCAACA TGCTCACTCC CTTAACATCTGT CCGTCTAGAG GTTTGGCTTC 180
TACAAACCAA GGGAGTCGAC GAGTTGAAG ATG AAG CCC AGA GCG GAG TGC TGT 233
Met Lys Pro Arg Ala Glu Cys Cys
1 5

TCT CCC AAG TTC TGG TTG GTG TTG GCC GTC CTG GCC GTG TCA GGC AGC 281
Ser Pro Lys Phe Trp Leu Val Leu Ala Val Leu Val Ser Gly Ser
10 15 20

AGA GCT CGT TCT CAG AAG AGC CCC CCC AGC ATT GGC ATT GCT GTC ATC 329
Arg Ala Arg Ser Gln Lys Ser Pro Pro Ser Ile Gly Ile Ala Val Ile
25 30 35 40

CTC GTG GGC ACT TCC GAC GAG GTG GCC ATC AAG GAT GCC CAC GAG AAA Leu Val Gly Thr Ser Asp Glu Val Ala Ile Lys Asp Ala His Glu Lys 45 50 55	377
GAT GAT TTC CAC CAT CTC TCC GTG GTA CCC CGG GTG GAA CTG GTA GCC Asp Asp Phe His His Leu Ser Val Val Pro Arg Val Glu Leu Val Ala 60 65 70	425
ATG AAT GAG ACC GAC CCA AAG AGC ATC ATC ACC CGC ATC TGT GAT CTC Met Asn Glu Thr Asp Pro Lys Ser Ile Ile Thr Arg Ile Cys Asp Leu 75 80 85	473
ATG TCT GAC CGG AAG ATC CAG GGG GTG GTG TTT GCT GAT GAC ACA GAC Met Ser Asp Arg Lys Ile Gln Gly Val Val Phe Ala Asp Asp Thr Asp 90 95 100	521
CAG GAA GCT ATC GCC CAG ATC CTC GAT TTC ATT TCA GCA CAG ACT CTC Gln Glu Ala Ile Ala Gln Ile Leu Asp Phe Ile Ser Ala Gln Thr Leu 105 110 115 120	569
ACC CCG ATC CTG GGC ATC CAC GGG GGC TCC TCT ATG ATA ATG GCA GAT Thr Pro Ile Leu Gly Ile His Gly Ser Ser Met Ile Met Ala Asp 125 130 135	617
AAG GAT GAA TCC TCC ATG TTC TTC CAG TTT GGC CCA TCA ATT GAA CAG Lys Asp Glu Ser Ser Met Phe Phe Gln Phe Gly Pro Ser Ile Glu Gln 140 145 150	665
CAA GCT TCC GTA ATG CTC AAC ATC ATG GAA GAA TAT GAC TGG TAC ATC Gln Ala Ser Val Met Leu Asn Ile Met Glu Glu Tyr Asp Trp Tyr Ile 155 160 165	713
TTT TCT ATC GTC ACC ACC TAT TTC CCT GGC TAC CAG GAC TTT GTA AAC Phe Ser Ile Val Thr Tyr Phe Pro Gly Tyr Gln Asp Phe Val Asn 170 175 180	761
AAG ATC CGC AGC ACC ATT GAG AAT AGC TTT GTG GGC TGG GAG CTA GAG Lys Ile Arg Ser Thr Ile Glu Asn Ser Phe Val Gly Trp Glu Leu Glu 185 190 195 200	809
GAG GTC CTC CTA CTG GAC ATG TCC CTG GAC GAT GGA GAT TCT AAG ATC Glu Val Leu Leu Asp Met Ser Leu Asp Asp Gly Asp Ser Lys Ile 205 210 215	857
CAG AAT CAG CTC AAG AAA CTT CAA AGC CCC ATC ATT CTT CTT TAC TGT Gln Asn Gln Leu Lys Leu Gln Ser Pro Ile Ile Leu Leu Tyr Cys 220 225 230	905
ACC AAG GAA GAA GCC ACC TAC ATC TTT GAA GTG GCC AAC TCA GTA GGG Thr Lys Glu Glu Ala Thr Tyr Ile Phe Glu Val Ala Asn Ser Val Gly 235 240 245	953
CTG ACT GGC TAT GGC TAC ACG TGG ATC GTG CCC AGT CTG GTG GCA GGG Leu Thr Gly Tyr Gly Tyr Thr Trp Ile Val Pro Ser Leu Val Ala Gly 250 255 260	1001
GAT ACA GAC ACA GTG CCT GCG GAG TTC CCC ACT GGG CTC ATC TCT GTA Asp Thr Asp Thr Val Pro Ala Glu Phe Pro Thr Gly Leu Ile Ser Val 265 270 275 280	1049
TCA TAT GAT GAA TGG GAC TAT GGC CTC CCC AGA GTG AGA GAT GGA Ser Tyr Asp Glu Trp Asp Tyr Gly Leu Pro Pro Arg Val Arg Asp Gly 285 290 295	1097
ATT GCC ATA ATC ACC ACT GCT GCT TCT GAC ATG CTG TCT GAG CAC AGC Ile Ala Ile Ile Thr Thr Ala Ala Ser Asp Met Leu Ser Glu His Ser 300 305 310	1145

TTC ATC CCT GAG CCC AAA AGC AGT TGT TAC AAC ACC CAJ GAS AAG AGA Phe Ile Pro Glu Pro Lys Ser Ser Cys Tyr Asn Thr His Glu Lys Arg 315 320 325	1193
ATC TAC CAG TCC AAT ATG CTA AAT AGG TAT CTG ATC AAT GTC ACT TTT Ile Tyr Gln Ser Asn Met Leu Asn Arg Tyr Leu Ile Asn Val Thr Phe 330 335 340	1241
GAG GGG AGG AAT TTG TCC TTC AGT GAA GAT GGC TAC CAG ATG CAC CCG Glu Gly Arg Asn Leu Ser Phe Ser Glu Asp Gly Tyr Gln Met His Pro 345 350 355 360	1289
AAA CTG GTG ATA ATT CTT CTG AAC AAG GAG AGG AAG TGG GAA AGG GTG Lys Leu Val Ile Ile Leu Asn Lys Glu Arg Lys Trp Glu Arg Val 365 370 375	1337
GGG AAG TGG AAA GAC AAG TCC CTG CAG ATG AAG TAC TAT GTG TGG CCC Gly Lys Trp Lys Asp Lys Ser Leu Gln Met Lys Tyr Tyr Val Trp Pro 380 385 390	1385
CGA ATG TGT CCA GAG ACT GAA GAG CAG GAG GAT GAC CAT CTG AGC ATT Arg Met Cys Pro Glu Thr Glu Gln Glu Asp Asp His Leu Ser Ile 395 400 405	1433
GTG ACC CTG GAG GAG GCA CCA TTT GTC ATT GTG GAA AGT GTG GAC CCT Val Thr Leu Glu Glu Ala Pro Phe Val Ile Val Glu Ser Val Asp Pro 410 415 420	1481
CTG AGT GGA ACC TGC ATG AGG AAC ACA GTC CCC TGC CAA AAA CGC ATA Leu Ser Gly Thr Cys Met Arg Asn Thr Val Pro Cys Gln Lys Arg Ile 425 430 435 440	1529
GTC ACT GAG AAT AAA ACA GAC GAG CCG GGT TAC ATC AAA AAA TGC Val Thr Glu Asn Lys Thr Asp Glu Glu Pro Gly Tyr Ile Lys Lys Cys 445 450 455	1577
TGC AAG GGG TTC TGT ATT GAC ATC CTT AAG AAA ATT TCT AAA TCT GTG Cys Lys Gly Phe Cys Ile Asp Ile Leu Lys Lys Ile Ser Lys Ser Val 460 465 470	1625
AAG TTC ACC TAT GAC CTT TAC CTG GTT ACC AAT GGC AAG CAT GGG AAG Lys Phe Thr Tyr Asp Leu Tyr Leu Val Thr Asn Gly Lys His Gly Lys 475 480 485	1673
AAA ATC AAT GGA ACC TGG AAT GGT ATG ATT GGA GAG GTG GTC ATG AAG Lys Ile Asn Gly Thr Trp Asn Gly Met Ile Gly Glu Val Val Met Lys 490 495 500	1721
AGG GCC TAC ATG GCA GTG GGC TCA CTC ACC ATC AAT GAG GAA CGA TCG Arg Ala Tyr Met Ala Val Gly Ser Leu Thr Ile Asn Glu Glu Arg Ser 505 510 515 520	1769
GAG GTG GTC GAC TTC TCT GTG CCC TTC ATA GAG ACA GGC ATC AGT GTC Glu Val Val Asp Phe Ser Val Pro Phe Ile Glu Thr Gly Ile Ser Val 525 530 535	1817
ATG GTG TCA CGC AGC AAT GGG ACT GTC TCA CCT TCT GCC TTC TTA GAG Met Val Ser Arg Ser Asn Gly Thr Val Ser Pro Ser Ala Phe Leu Glu 540 545 550	1865
CCA TTC AGC GCT GAC GTA TGG GTG ATG ATG TTT GTG ATG CTG CTC ATC Pro Phe Ser Ala Asp Val Trp Val Met Met Phe Val Met Leu Leu Ile 555 560 565	1913
GTC TCA GCC GTG GCT GTC TTT GTC TTT GAG TAC TTC AGC CCT GTG GGT Val Ser Ala Val Ala Val Phe Val Phe Glu Tyr Phe Ser Pro Val Gly 570 575 580	1961

TAT AAC AGG TGC CTC GCT GAT GGC AGA GAG CCT GGT GGA CCC TCT TTC Tyr Asn Arg Cys Leu Ala Asp Gly Arg Glu Pro Gly Gly Pro Ser Phe 585 590 595 600	2009
ACC ATC GGC AAA GCT ATT TGG TTG CTC TGG GGT CTG GTG TTT AAC AAC Thr Ile Gly Lys Ala Ile Trp Leu Leu Trp Gly Leu Val Phe Asn Asn 605 610 615	2057
TCC GTA CCT GTG CAG AAC CCA AAG GGG ACC ACC TCC AAG ATC ATG GTG Ser Val Pro Val Gln Asn Pro Lys Gly Thr Thr Ser Lys Ile Met Val 620 625 630	2105
TCA GTG TGG GCC TTC TTT GCT GTC ATC TTC CTG GCC AGC TAC ACT GCC Ser Val Trp Ala Phe Ala Val Ile Phe Leu Ala Ser Tyr Thr Ala 635 640 645	2153
AAC TTA GCT GCC TTC ATG ATC CAA GAG GAA TAT GTG GAC CAG GTT TCT Asn Leu Ala Ala Phe Met Ile Gln Glu Glu Tyr Val Asp Gln Val Ser 650 655 660	2201
GGC CTG AGC GAC AAA AAG TTC CAG AGA CCT AAT GAC TTC TCA CCC CCT Gly Leu Ser Asp Lys Lys Phe Gln Arg Pro Asn Asp Phe Ser Pro Pro 665 670 675 680	2249
TTC CGC TTT GGG ACC GTG CCC AAC GGC AGC ACA GAG AGA AAT ATT CGC Phe Arg Phe Gly Thr Val Pro Asn Gly Ser Thr Glu Arg Asn Ile Arg 685 690 695	2297
AAT AAC TAT GCA GAA ATG CAT GCC TAC ATG GGA AAG TTC AAC CAG AGG Asn Asn Tyr Ala Glu Met His Ala Tyr Met Gly Lys Phe Asn Gln Arg 700 705 710	2345
GGT GTA GAT GAT GCA TTG CTC TCC CTG AAA ACA GGG AAA CTG GAT GCC Gly Val Asp Asp Ala Leu Leu Ser Leu Lys Thr Gly Lys Leu Asp Ala 715 720 725	2393
TTC ATC TAT GAT GCA GCA GTG CTG AAC TAT ATG GCA GGC AGA GAT GAA Phe Ile Tyr Asp Ala Ala Val Leu Asn Tyr Met Ala Gly Arg Asp Glu 730 735 740	2441
GGC TGC AAG CTG GTG ACC ATT GGC AGT GGG AAG GTC TTT GCT TCC ACT Gly Cys Lys Leu Val Thr Ile Gly Ser Gly Lys Val Phe Ala Ser Thr 745 750 755 760	2489
GGC TAT GGC ATT GCC ATC CAA AAA GAT TCT GGG TGG AAG CGC CAG GTG Gly Tyr Gly Ile Ala Ile Gln Lys Asp Ser Gly Trp Lys Arg Gln Val 765 770 775	2537
GAC CTT GCT ATC CTG CAG CTC TTT GGA GAT GGG GAG ATG GAA GAA CTG Asp Leu Ala Ile Leu Gln Leu Phe Gly Asp Gly Glu Met Glu Glu Leu 780 785 790	2585
GAA GCT CTC TGG CTC ACT GGC ATT TGT CAC AAT GAG AAG AAT GAG GTC Glu Ala Leu Trp Leu Thr Gly Ile Cys His Asn Glu Lys Asn Glu Val 795 800 805	2633
ATG AGC AGC CAG CTG GAC ATT GAC AAC ATG GCA GGG GTC TTC TAC ATG Met Ser Ser Gln Leu Asp Ile Asp Asn Met Ala Gly Val Phe Tyr Met 810 815 820	2681
TTG GGG GCG GCC ATG GCT CTC AGC CTC ATC ACC TTC ATC TGC GAA CAC Leu Gly Ala Ala Met Ala Leu Ser Leu Ile Thr Phe Ile Cys Glu His 825 830 835 840	2729
CTT TTC TAT TGG CAG TTC CGA CAT TGC TTT ATG GGT GTC TGT TCT GGC Leu Phe Tyr Trp Gln Phe Arg His Cys Phe Met Gly Val Cys Ser Gly 845 850 855	2777

AAG CCT GGC ATG GTC TTC TCC ATC AGC AGA GGT ATC TAC AGC TGC ATC Lys Pro Gly Met Val Phe Ser Ile Ser Arg Gly Ile Tyr Ser Cys Ile 860 865 870	2825
CAT GGG GTG GCG ATC GAG GAG CGC CAG TCT GTA ATG AAC TCC CCC ACC His Gly Val Ala Ile Glu Glu Arg Gln Ser Val Met Asn Ser Pro Thr 875 880 885	2873
GCA ACC ATG AAC AAC ACA CAC TCC AAC ATC CTG CGC CTG CTG CGC ACG Ala Thr Met Asn Asn Thr His Ser Asn Ile Leu Arg Leu Leu Arg Thr 890 895 900	2921
GCC AAG AAC ATG GCT AAC CTG TCT GGT GTG AAT GGC TCA CCG CAG AGC Ala Lys Asn Met Ala Asn Leu Ser Gly Val Asn Gly Ser Pro Gln Ser 905 910 915 920	2969
GCC CTG GAC TTC ATC CGA CGG GAG TCA TCC GTC TAT GAC ATC TCA GAG Ala Leu Asp Phe Ile Arg Arg Glu Ser Ser Val Tyr Asp Ile Ser Glu 925 930 935	3017
CAC CGC CGC AGC TTC ACG CAT TCT GAC TGC AAA TCC TAC AAC AAC CCG His Arg Arg Ser Phe Thr His Ser Asp Cys Lys Ser Tyr Asn Asn Pro 940 945 950	3065
CCC TGT GAG GAG AAC CTC TTC AGT GAC TAC ATC AGT GAG GTA GAG AGA Pro Cys Glu Glu Asn Leu Phe Ser Asp Tyr Ile Ser Glu Val Glu Arg 955 960 965	3113
ACG TTC GGG AAC CTG CAG CTG AAG GAC AGC AAC GTG TAC CAA GAT CAC Thr Phe Gly Asn Leu Gln Leu Lys Asp Ser Asn Val Tyr Gln Asp His 970 975 980	3161
TAC CAC CAT CAC CAC CGG CCC CAT AGT ATT GGC AGT GCC AGC TCC ATC Tyr His His His His Arg Pro His Ser Ile Gly Ser Ala Ser Ser Ile 985 990 995 1000	3209
GAT GGG CTC TAC GAC TGT GAC AAC CCA CCC TTC ACC ACC CAG TCC AGG Asp Gly Leu Tyr Asp Cys Asp Asn Pro Pro Phe Thr Thr Gln Ser Arg 1005 1010 1015	3257
TCC ATC AGC AAG AAG CCC CTG GAC ATC GGC CTC CCC TCC TCC AAG CAC Ser Ile Ser Lys Lys Pro Leu Asp Ile Gly Leu Pro Ser Ser Lys His 1020 1025 1030	3305
AGC CAG CTC AGT GAC CTG TAC GGC AAA TTC TCC TTC AAG AGC GAC CGC Ser Gln Leu Ser Asp Leu Tyr Gly Lys Phe Ser Phe Lys Ser Asp Arg 1035 1040 1045	3353
TAC AGT GGC CAC GAC GAC TTG ATC CGC TCC GAT GTC TCT GAC ATC TCA Tyr Ser Gly His Asp Asp Leu Ile Arg Ser Asp Val Ser Asp Ile Ser 1050 1055 1060	3401
ACC CAC ACC GTC ACC TAT GGG AAC ATC GAG GGC AAT GCC GCC AAG AGG Thr His Thr Val Thr Tyr Gly Asn Ile Glu Gly Asn Ala Ala Lys Arg 1065 1070 1075 1080	3449
CGT AAG CAG CAA TAT AAG GAC AGC CTG AAG AAG CGG CCT GCC TCG GCC Arg Lys Gln Gln Tyr Lys Asp Ser Leu Lys Lys Arg Pro Ala Ser Ala 1085 1090 1095	3497
AAG TCC CGC AGG GAG TTT GAC GAG ATC GAG CTG GCC TAC CGT CGC CGA Lys Ser Arg Arg Glu Phe Asp Glu Ile Glu Leu Ala Tyr Arg Arg Arg 1100 1105 1110	3545
CCG CCC CGC TCC CCT GAC CAC AAG CGC TAC TTC AGG GAC AAG GAA GGG Pro Pro Arg Ser Pro Asp His Lys Arg Tyr Phe Arg Asp Lys Glu Gly 1115 1120 1125	3593

CTA CGG GAC TTC TAC CTG GAC CAG TTC CGA ACA AAG GAG AAC TCA CCC Leu Arg Asp Phe Tyr Leu Asp Gln Phe Arg Thr Lys Glu Asn Ser Pro 1130 1135 1140	3641
CAC TGG GAG CAC GTA GAC CTG ACC GAC ATC TAC AAG GAG CGG AGT GAT His Trp Glu His Val Asp Leu Thr Asp Ile Tyr Lys Glu Arg Ser Asp 1145 1150 1155 1160	3689
GAC TTT AAG CGC GAC TCC ATC AGC GGA GGA GGG CCC TGT ACC AAC AGG Asp Phe Lys Arg Asp Ser Ile Ser Gly Gly Gly Pro Cys Thr Asn Arg 1165 1170 1175	3737
TCT CAC ATC AAG CAC GGG ACG GGC GAC AAA CAC GGC GTG GTC AGC GGG Ser His Ile Lys His Gly Thr Gly Asp Lys His Gly Val Val Ser Gly 1180 1185 1190	3785
GTA CCT GCA CCT TGG GAG AAG AAC CTG ACC AAC GTG GAG TGG GAG GAC Val Pro Ala Pro Trp Glu Lys Asn Leu Thr Asn Val Glu Trp Glu Asp 1195 1200 1205	3833
CGG TCC GGG GGC AAC TTC TGC CGC AGC TGT CCC TCC AAG CTG CAC AAC Arg Ser Gly Gly Asn Phe Cys Arg Ser Cys Pro Ser Lys Leu His Asn 1210 1215 1220	3881
TAC TCC ACG ACG GTG ACG GGT CAG AAC TCG GGC AGG CAG GCG TGC ATC Tyr Ser Thr Thr Val Thr Gly Gln Asn Ser Gly Arg Gln Ala Cys Ile 1225 1230 1235 1240	3929
CGG TGT GAG GCT TGC AAG AAA GCA GGC AAC CTG TAT GAC ATC AGT GAG Arg Cys Glu Ala Cys Lys Lys Ala Gly Asn Leu Tyr Asp Ile Ser Glu 1245 1250 1255	3977
GAC AAC TCC CTG CAG GAA CTG GAC CAG CCG GCT GCC CCA GTG GCG GTG Asp Asn Ser Leu Gln Glu Leu Asp Gln Pro Ala Ala Pro Val Ala Val 1260 1265 1270	4025
ACG TCA AAC GCC TCC ACC ACT AAG TAC CCT CAG AGC CCG ACT AAT TCC Thr Ser Asn Ala Ser Thr Thr Lys Tyr Pro Gln Ser Pro Thr Asn Ser 1275 1280 1285	4073
AAG GCC CAG AAG AAG AAC CGG AAC AAA CTG CGC CGG CAG CAC TCC TAC Lys Ala Gln Lys Lys Asn Arg Asn Lys Leu Arg Arg Gln His Ser Tyr 1290 1295 1300	4121
GAC ACC TTC GTG GAC CTG CAG AAG GAA GAA GCC GCC CTG GCC CCG CGC Asp Thr Phe Val Asp Leu Gln Lys Glu Ala Ala Leu Ala Pro Arg 1305 1310 1315 1320	4169
AGC GTA AGC CTG AAA GAC AAG GGC CGA TTC ATG GAT GGG AGC CCC TAC Ser Val Ser Leu Lys Asp Lys Gly Arg Phe Met Asp Gly Ser Pro Tyr 1325 1330 1335	4217
GCC CAC ATG TTT GAG ATG TCA GCT GGC GAG AGC ACC TTT GCC AAC AAC Ala His Met Phe Glu Met Ser Ala Gly Glu Ser Thr Phe Ala Asn Asn 1340 1345 1350	4265
AAG TCC TCA GTG CCC ACT GCC GGA CAT CAC CAC AAC AAC CCC GGC Lys Ser Ser Val Pro Thr Ala Gly His His His Asn Asn Pro Gly 1355 1360 1365	4313
GGC GGG TAC ATG CTC AGC AAG TCG CTC TAC CCT GAC CGG GTC ACG CAA Gly Gly Tyr Met Leu Ser Lys Ser Leu Tyr Pro Asp Arg Val Thr Gln 1370 1375 1380	4361
AAC CCT TTC ATC CCC ACT TTT GGG GAC GAC CAG TGC TTG CTC CAT GGC Asn Pro Phe Ile Pro Thr Phe Gly Asp Asp Gln Cys Leu Leu His Gly 1385 1390 1395 1400	4409

AGC AAA TCC TAC TTC AGG CAG CCC ACG GTG GCG GGG GCG TCG AAA Ser Lys Ser Tyr Phe Phe Arg Gln Pro Thr Val Ala Gly Ala Ser Lys 1405 1410 1415	4457
GCC AGG CCG GAC TTC CGG GCC CTT GTC ACC AAC AAG CCG GTG GTC TCG Ala Arg Pro Asp Phe Arg Ala Leu Val Thr Asn Lys Pro Val Val Ser 1420 1425 1430	4505
GCC CTT CAT GGG GCC GTG CCA GCC CGT TTC CAG AAG GAC ATC TGT ATA Ala Leu His Gly Ala Val Pro Ala Arg Phe Gln Lys Asp Ile Cys Ile 1435 1440 1445	4553
GGG AAC CAG TCC AAC CCC TGT GTG CCT AAC AAC ACA AAC CCC AGG GCT Gly Asn Gln Ser Asn Pro Cys Val Pro Asn Asn Thr Asn Pro Arg Ala 1450 1455 1460	4601
TTC AAT GGC TCC AGC AAT GGG CAT GTT TAT GAG AAA CTT TCT AGT ATT Phe Asn Gly Ser Ser Asn Gly His Val Tyr Glu Lys Leu Ser Ser Ile 1465 1470 1475 1480	4649
GAG TCT GAT GTC TGAGTGAGGG AACAGAGAGG TTAAGGTGGG TACGGGAGGG Glu Ser Asp Val 148	4701
TAAGGCTGTG GGTCGCGTGA TCGCATGTC ACGGAGGGTG ACGGGGGTGA ACTTGGTTCC CATTGCTCC TTTCTTGTAA TAAATTATTT ATGGGATCCT GGAGTTCTGG TTCTACTGG GGGCAACCTT GGTGACCAGC ACCATCTCTC CTCCTTTCA CAGTTCTCTC CTTCTTCCCC CCGCTGTGAG CCATTCCTGT TCCCAGAGA TGATGCCATG GGCCCTCTGA GCAGGGAGG GTAGAGCGGA GAAAGGAAGG GCTGCATGCG GGCTTCCTCC TGGTGTGGAA GAGCTCTTG ATATCCTCTT TGAGTGAAGC TGGGAGAACCC AAAAAGAGGC TATGTGAGCA CAAAGGTAGC TTTTCCAAA CTGATCTTTT CATTAGGTG AGGAAGCAAA AGCATCTATG TGAGACCATT TAGCACACTG CTTGTGAAAG GAAAGAGGCT CTGGCTAAAT TCATGCTGCT TAGATGACAT CTGTCTAGGA ATCATGTGCC AAGCAGAGGT TGGGAGGCCA TTTGTGTTA TATATAAGCC AAAAATGCT TGCTTCAACC CCATGAGACT CGATAGTGGT GGTGAACAGA ACCCAAGGTC ATTGGTGGCA GAGTGGATTG TTGAACAAAC TGGAAAGTAC GTTATGATAG TGTCCCCCGG TGCCTTGGGG ACAAGAGCAG GTGGATTGTG CGTGCATGTG TGTTCATGCA CACTTGCACC CATGTGAGT CAGGTGCCTC AAGAGAAGGC AACCTTGACT CTTTCGTTGA ATTTGCATCT CTTCAAGACA CAAGATTAAA ACAAAATTAA CGCTAAATTG GATTTAAAT TATCTTC	4761 4821 4881 4941 5001 5061 5121 5181 5241 5301 5361 5421 5481 5538

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1484 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Met Lys Pro Arg Ala Glu Cys Cys Ser Pro Lys Phe Trp Leu Val Leu
1 5 10 15

Ala Val Leu Ala Val Ser Gly Ser Arg Ala Arg Ser Gln Lys Ser Pro
20 25 30

Pro Ser Ile Gly Ile Ala Val Ile Leu Val Gly Thr Ser Asp Glu Val
35 40 45

Ala Ile Lys Asp Ala His Glu Lys Asp Asp Phe His His Leu Ser Val
50 55 60

Val Pro Arg Val Glu Leu Val Ala Met Asn Glu Thr Asp Pro Lys Ser
65 70 75 80

Ile Ile Thr Arg Ile Cys Asp Leu Met Ser Asp Arg Lys Ile Gln Gly
85 90 95

Val Val Phe Ala Asp Asp Thr Asp Gln Glu Ala Ile Ala Gln Ile Leu
100 105 110

Asp Phe Ile Ser Ala Gln Thr Leu Thr Pro Ile Leu Gly Ile His Gly
115 120 125

Gly Ser Ser Met Ile Met Ala Asp Lys Asp Glu Ser Ser Met Phe Phe
130 135 140

Gln Phe Gly Pro Ser Ile Glu Gln Gln Ala Ser Val Met Leu Asn Ile
145 150 155 160

Met Glu Glu Tyr Asp Trp Tyr Ile Phe Ser Ile Val Thr Thr Tyr Phe
165 170 175

Pro Gly Tyr Gln Asp Phe Val Asn Lys Ile Arg Ser Thr Ile Glu Asn
180 185 190

Ser Phe Val Gly Trp Glu Leu Glu Val Leu Leu Leu Asp Met Ser
195 200 205

Leu Asp Asp Gly Asp Ser Lys Ile Gln Asn Gln Leu Lys Lys Leu Gln
210 215 220

Ser Pro Ile Ile Leu Leu Tyr Cys Thr Lys Glu Glu Ala Thr Tyr Ile
225 230 235 240

Phe Glu Val Ala Asn Ser Val Gly Leu Thr Gly Tyr Gly Tyr Thr Trp
245 250 255

Ile Val Pro Ser Leu Val Ala Gly Asp Thr Asp Thr Val Pro Ala Glu
260 265 270

Phe Pro Thr Gly Leu Ile Ser Val Ser Tyr Asp Glu Trp Asp Tyr Gly
275 280 285

Leu Pro Pro Arg Val Arg Asp Gly Ile Ala Ile Ile Thr Thr Ala Ala
290 295 300

Ser Asp Met Leu Ser Glu His Ser Phe Ile Pro Glu Pro Lys Ser Ser
305 310 315 320

Cys Tyr Asn Thr His Glu Lys Arg Ile Tyr Gln Ser Asn Met Leu Asn
325 330 335

Arg Tyr Leu Ile Asn Val Thr Phe Glu Gly Arg Asn Leu Ser Phe Ser
340 345 350

Glu Asp Gly Tyr Gln Met His Pro Lys Leu Val Ile Ile Leu Leu Asn
355 360 365

Lys Glu Arg Lys Trp Glu Arg Val Gly Lys Trp Lys Asp Lys Ser Leu

370	375	380
Gln Met Lys Tyr Tyr Val Trp Pro Arg Met Cys Pro Glu Thr Glu Glu		
385	390	395
400		
Gln Glu Asp Asp His Leu Ser Ile Val Thr Leu Glu Glu Ala Pro Phe		
405	410	415
Val Ile Val Glu Ser Val Asp Pro Leu Ser Gly Thr Cys Met Arg Asn		
420	425	430
Thr Val Pro Cys Gln Lys Arg Ile Val Thr Glu Asn Lys Thr Asp Glu		
435	440	445
Glu Pro Gly Tyr Ile Lys Lys Cys Cys Lys Gly Phe Cys Ile Asp Ile		
450	455	460
Leu Lys Lys Ile Ser Lys Ser Val Lys Phe Thr Tyr Asp Leu Tyr Leu		
465	470	475
480		
Val Thr Asn Gly Lys His Gly Lys Ile Asn Gly Thr Trp Asn Gly		
485	490	495
Met Ile Gly Glu Val Val Met Lys Arg Ala Tyr Met Ala Val Gly Ser		
500	505	510
Leu Thr Ile Asn Glu Glu Arg Ser Glu Val Val Asp Phe Ser Val Pro		
515	520	525
Phe Ile Glu Thr Gly Ile Ser Val Met Val Ser Arg Ser Asn Gly Thr		
530	535	540
Val Ser Pro Ser Ala Phe Leu Glu Pro Phe Ser Ala Asp Val Trp Val		
545	550	555
560		
Met Met Phe Val Met Leu Leu Ile Val Ser Ala Val Ala Val Phe Val		
565	570	575
Phe Glu Tyr Phe Ser Pro Val Gly Tyr Asn Arg Cys Leu Ala Asp Gly		
580	585	590
Arg Glu Pro Gly Gly Pro Ser Phe Thr Ile Gly Lys Ala Ile Trp Leu		
595	600	605
Leu Trp Gly Leu Val Phe Asn Asn Ser Val Pro Val Gln Asn Pro Lys		
610	615	620
Gly Thr Thr Ser Lys Ile Met Val Ser Val Trp Ala Phe Phe Ala Val		
625	630	635
640		
Ile Phe Leu Ala Ser Tyr Thr Ala Asn Leu Ala Ala Phe Met Ile Gln		
645	650	655
Glu Glu Tyr Val Asp Gln Val Ser Gly Leu Ser Asp Lys Lys Phe Gln		
660	665	670
Arg Pro Asn Asp Phe Ser Pro Pro Phe Arg Phe Gly Thr Val Pro Asn		
675	680	685
Gly Ser Thr Glu Arg Asn Ile Arg Asn Asn Tyr Ala Glu Met His Ala		
690	695	700
Tyr Met Gly Lys Phe Asn Gln Arg Gly Val Asp Asp Ala Leu Leu Ser		
705	710	715
720		
Leu Lys Thr Gly Lys Leu Asp Ala Phe Ile Tyr Asp Ala Ala Val Leu		
725	730	735

Asn Tyr Met Ala Gly Arg Asp Glu Gly Cys Lys Leu Val Thr Ile Gly
740 745 750

Ser Gly Lys Val Phe Ala Ser Thr Gly Tyr Gly Ile Ala Ile Gln Lys
755 760 765

Asp Ser Gly Trp Lys Arg Gln Val Asp Leu Ala Ile Leu Gln Leu Phe
770 775 780

Gly Asp Gly Glu Met Glu Glu Leu Glu Ala Leu Trp Leu Thr Gly Ile
785 790 795 800

Cys His Asn Glu Lys Asn Glu Val Met Ser Ser Gln Leu Asp Ile Asp
805 810 815

Asn Met Ala Gly Val Phe Tyr Met Leu Gly Ala Ala Met Ala Leu Ser
820 825 830

Leu Ile Thr Phe Ile Cys Glu His Leu Phe Tyr Trp Gln Phe Arg His
835 840 845

Cys Phe Met Gly Val Cys Ser Gly Lys Pro Gly Met Val Phe Ser Ile
850 855 860

Ser Arg Gly Ile Tyr Ser Cys Ile His Gly Val Ala Ile Glu Glu Arg
865 870 875 880

Gln Ser Val Met Asn Ser Pro Thr Ala Thr Met Asn Asn Thr His Ser
885 890 895

Asn Ile Leu Arg Leu Leu Arg Thr Ala Lys Asn Met Ala Asn Leu Ser
900 905 910

Gly Val Asn Gly Ser Pro Gln Ser Ala Leu Asp Phe Ile Arg Arg Glu
915 920 925

Ser Ser Val Tyr Asp Ile Ser Glu His Arg Arg Ser Phe Thr His Ser
930 935 940

Asp Cys Lys Ser Tyr Asn Asn Pro Pro Cys Glu Glu Asn Leu Phe Ser
945 950 955 960

Asp Tyr Ile Ser Glu Val Glu Arg Thr Phe Gly Asn Leu Gln Leu Lys
965 970 975

Asp Ser Asn Val Tyr Gln Asp His Tyr His His His Arg Pro His
980 985 990

Ser Ile Gly Ser Ala Ser Ser Ile Asp Gly Leu Tyr Asp Cys Asp Asn
995 1000 1005

Pro Pro Phe Thr Thr Gln Ser Arg Ser Ile Ser Lys Lys Pro Leu Asp
1010 1015 1020

Ile Gly Leu Pro Ser Ser Lys His Ser Gln Leu Ser Asp Leu Tyr Gly
1025 1030 1035 1040

Lys Phe Ser Phe Lys Ser Asp Arg Tyr Ser Gly His Asp Asp Leu Ile
1045 1050 1055

Arg Ser Asp Val Ser Asp Ile Ser Thr His Thr Val Thr Tyr Gly Asn
1060 1065 1070

Ile Glu Gly Asn Ala Ala Lys Arg Arg Lys Gln Gln Tyr Lys Asp Ser
1075 1080 1085

Leu Lys Lys Arg Pro Ala Ser Ala Lys Ser Arg Arg Glu Phe Asp Glu

1090

1095

1100

Ile Glu Leu Ala Tyr Arg Arg Arg Pro Pro Arg Ser Pro Asp His Lys
1105 1110 1115 1120

Arg Tyr Phe Arg Asp Lys Glu Gly Leu Arg Asp Phe Tyr Leu Asp Gln
1125 1130 1135

Phe Arg Thr Lys Glu Asn Ser Pro His Trp Glu His Val Asp Leu Thr
1140 1145 1150

Asp Ile Tyr Lys Glu Arg Ser Asp Asp Phe Lys Arg Asp Ser Ile Ser
1155 1160 1165

Gly Gly Gly Pro Cys Thr Asn Arg Ser His Ile Lys His Gly Thr Gly
1170 1175 1180

Asp Lys His Gly Val Val Ser Gly Val Pro Ala Pro Trp Glu Lys Asn
1185 1190 1195 1200

Leu Thr Asn Val Glu Trp Glu Asp Arg Ser Gly Gly Asn Phe Cys Arg
1205 1210 1215

Ser Cys Pro Ser Lys Leu His Asn Tyr Ser Thr Thr Val Thr Gly Gln
1220 1225 1230

Asn Ser Gly Arg Gln Ala Cys Ile Arg Cys Glu Ala Cys Lys Lys Ala
1235 1240 1245

Gly Asn Leu Tyr Asp Ile Ser Glu Asp Asn Ser Leu Gln Glu Leu Asp
1250 1255 1260

Gln Pro Ala Ala Pro Val Ala Val Thr Ser Asn Ala Ser Thr Thr Lys
1265 1270 1275 1280

Tyr Pro Gln Ser Pro Thr Asn Ser Lys Ala Gln Lys Lys Asn Arg Asn
1285 1290 1295

Lys Leu Arg Arg Gln His Ser Tyr Asp Thr Phe Val Asp Leu Gln Lys
1300 1305 1310

Glu Glu Ala Ala Leu Ala Pro Arg Ser Val Ser Leu Lys Asp Lys Gly
1315 1320 1325

Arg Phe Met Asp Gly Ser Pro Tyr Ala His Met Phe Glu Met Ser Ala
1330 1335 1340

Gly Glu Ser Thr Phe Ala Asn Asn Lys Ser Ser Val Pro Thr Ala Gly
1345 1350 1355 1360

His His His Asn Asn Pro Gly Gly Tyr Met Leu Ser Lys Ser
1365 1370 1375

Leu Tyr Pro Asp Arg Val Thr Gln Asn Pro Phe Ile Pro Thr Phe Gly
1380 1385 1390

Asp Asp Gln Cys Leu Leu His Gly Ser Lys Ser Tyr Phe Phe Arg Gln
1395 1400 1405

Pro Thr Val Ala Gly Ala Ser Lys Ala Arg Pro Asp Phe Arg Ala Leu
1410 1415 1420

Val Thr Asn Lys Pro Val Val Ser Ala Leu His Gly Ala Val Pro Ala
1425 1430 1435 1440

Arg Phe Gln Lys Asp Ile Cys Ile Gly Asn Gln Ser Asn Pro Cys Val
1445 1450 1455

Pro Asn Asn Thr Asn Pro Arg Ala Phe Asn Gly Ser Ser Asn Gly His
1450 1465 1470

Val Tyr Glu Lys Leu Ser Ser Ile Glu Ser Asp Val
1475 1480

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4695 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 485..4495

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

CGAGAACACA GCGAGTGTGT GAGTCCTCC CGCTCCAGCT CCTCCAAGCC GCGGCCGCCG	60
CGGCCACCCCT CGCCCGCAGC CTCCCGCAGC CTCCCTCGGC CACCGGTGTC TGGTGGGGT	120
GTTGCCTGGG TAGGTCGGCC CGGCCCCCAG GGGTCTCTCG AGCGTCTGCC ATCTGCCGA	180
GAAACATGTG TGGCCACGTC CTCGCCTAGT CCAGGTGGCC GCAACCTTGG GGGAGAGACA	240
GGGCAGGACA GGACCAAGGT AAGAGGTAAG GAGGAGACGG CGCCAGGGAC AGACAGGAGG	300
TCCCGGCTTG CGCTTGTGCG CACCACACT GCCGCCGCC CGGGGCTGTC CCCCACATC	360
GGCTCTCTGA GCCCTCCTCG GAATCTTGGG GTCGCTGGAC GCCGGGTTCC GGTCTGGCC	420
CCCCCCCAT CCCCCCAACA GAACAGGGTC ATGAAAAGAG GCCGCCCGGC GGGGCCCGCA	480
GGCG ATG CGC GGC GCC GGT GGC CCC CGC GGC CCT CGG GGC CCC GCT AAG Met Arg Gly Ala Gly Gly Pro Arg Gly Pro Arg Gly Pro Ala Lys	529
1 5 10 15	
ATG CTG CTG CTG GCG CTG GCC TGC AGC CCG TTC CCG GAG GAG Met Leu Leu Leu Ala Leu Ala Cys Ala Ser Pro Phe Pro Glu Glu	577
20 25 30	
GCG CCG GGG CCG GGC GGG GGT GGG CCC GGC GGC CTC GGC GGG Ala Pro Gly Pro Gly Ala Gly Gly Pro Gly Gly Leu Gly Gly	625
35 40 45	
GCG CGG CCG CTC AAC GTG GCG CTC GTG TTC TCG GGG CCC GCG TAC GCG Ala Arg Pro Leu Asn Val Ala Leu Val Phe Ser Gly Pro Ala Tyr Ala	673
50 55 60	
GCC GAG GCG GCA CGC CTG GGC CCG GCC GTG GCG GCG GCG GTG CGC AGC Ala Glu Ala Ala Arg Leu Gly Pro Ala Val Ala Ala Val Arg Ser	721
65 70 75	
CCG GGC CTA GAC GTG CGG CCC GTG GCG CTG GTG CTC AAC GGC TCG GAC Pro Gly Leu Asp Val Arg Pro Val Ala Leu Val Leu Asn Gly Ser Asp	769
80 85 90 95	
CCG CGC AGC CTC GTG CTG CAG CTC TGC GAC CTG CTG TCG GGG TTG CGC Pro Arg Ser Leu Val Leu Gln Leu Cys Asp Leu Ser Gly Leu Arg	817

	100	105	110	
GTG CAC GGC GTG GTC TTC GAA GAC GAC TCG CGC GCG CCC GCC GTC GCG Val His Gly Val Val Phe Glu Asp Asp Ser Arg Ala Pro Ala Val Ala	115	120	125	865
CCC ATC CTC GAC TTC CTG TCG GCG CAG ACC TCG CTC CCC ATC GTG TCC Pro Ile Leu Asp Phe Leu Ser Ala Gln Thr Ser Leu Pro Ile Val Ser	130	135	140	913
GAG CAC GGC GGC GCC GCG CTC GTG CTC ACG CCC AAG GAG AAG GGC TCC Glu His Gly Gly Ala Ala Leu Val Leu Thr Pro Lys Glu Lys Gly Ser	145	150	155	961
ACC TTC CTC CAC CTG GGC TCT TCC CCC GAG CAA CAG CTT CAG GTC ATC Thr Phe Leu His Leu Gly Ser Ser Pro Glu Gln Gln Leu Gln Val Ile	160	165	170	1009
TTT GAG GTG CTG GAG GAG TAT GAC TGG ACG TCC TTT GTA GCC GTG ACC Phe Glu Val Leu Glu Glu Tyr Asp Trp Thr Ser Phe Val Ala Val Thr	180	185	190	1057
ACT CGT GCC CCT GGC CAC CGG GCC TTC CTG TCC TAC ATT GAG GTG CTG Thr Arg Ala Pro Gly His Arg Ala Phe Leu Ser Tyr Ile Glu Val Leu	195	200	205	1105
ACT GAC GGC AGT CTG GTG GGC TGG GAG CAC CGC GGA GCG CTG ACG CTG Thr Asp Gly Ser Leu Val Gly Trp Glu His Arg Gly Ala Leu Thr Leu	210	215	220	1153
GAC CCT GGG GCG GGC GAG GCC GTG CTC AGT GCC CAG CTC CGC AGT GTC Asp Pro Gly Ala Gly Glu Ala Val Leu Ser Ala Gln Leu Arg Ser Val	225	230	235	1201
AGC GCG CAG ATC CGC CTG CTC TTC TGC GCC CGA GAG GAG GCC GAG CCC Ser Ala Gln Ile Arg Leu Leu Phe Cys Ala Arg Glu Glu Ala Glu Pro	240	245	250	1249
GTG TTC CGC GCA GCT GAG GAG GCT GGC CTC ACT GGA TCT GGC TAC GTC Val Phe Arg Ala Ala Glu Glu Ala Gly Leu Thr Gly Ser Gly Tyr Val	260	265	270	1297
TGG TTC ATG GTG GGG CCC CAG CTG GCT GGA GGC GGG GGC TCT GGG GCC Trp Phe Met Val Gly Pro Gln Leu Ala Gly Gly Gly Ser Gly Ala	275	280	285	1345
CCT GGT GAG CCC CCT CTT CTG CCA GGA GGC GCC CCC CTG CCT GCC GGG Pro Gly Glu Pro Pro Leu Leu Pro Gly Gly Ala Pro Leu Pro Ala Gly	290	295	300	1393
CTG TTT GCA GTG CGC TCG GCT GGC TGG CGG GAT GAC CTG GCT CGG CGA Leu Phe Ala Val Arg Ser Ala Gly Trp Arg Asp Asp Leu Ala Arg Arg	305	310	315	1441
GTG GCA GCT GGC GTG GCC GTA GTG GCC AGA GGT GCC CAG GCC CTG CTG Val Ala Ala Gly Val Ala Val Ala Arg Gly Ala Gln Ala Leu Leu	320	325	330	1489
CGT GAT TAT GGT TTC CTT CCT GAG CTC GGC CAC GAC TGT CGC GCC CAG Arg Asp Tyr Gly Phe Leu Pro Glu Leu Gly His Asp Cys Arg Ala Gln	340	345	350	1537
AAC CGC ACC CAC CGC GGG GAG AGT CTG CAT AGG TAC TTC ATG AAC ATC Asn Arg Thr His Arg Gly Glu Ser Leu His Arg Tyr Phe Met Asn Ile	355	360	365	1585
ACG TGG GAT AAC CGG GAT TAC TCC AAT GAG GAC GGC TTC CTA GTG				1633

Thr Trp Asp Asn Arg Asp Tyr Ser Phe Asn Glu Asp Gly Phe Leu Val			
370	375	380	
AAC CCC TCC CTG GTG GTC ATC TCC CTC ACC AGA GAC AGG ACG TGG GAG		1681	
Asn Pro Ser Leu Val Val Ile Ser Leu Thr Arg Asp Arg Thr Trp Glu			
385	390	395	
G TG GGC AGC TGG GAG CAG CAG ACG CTC CGC CTC AAG TAC CCG CTG		1729	
Val Val Gly Ser Trp Glu Gln Gln Thr Leu Arg Leu Lys Tyr Pro Leu			
400	405	410	415
TGG TCC CGC TAT GGT CGC TTC CTG CAG CCA GTG GAC GAC ACG CAG CAC		1777	
Trp Ser Arg Tyr Gly Arg Phe Leu Gln Pro Val Asp Asp Thr Gln His			
420	425	430	
CTC GCG GTG GCC ACG CTG GAG GAA AGG CCG TTT GTC ATC GTG GAG CCT		1825	
Leu Ala Val Ala Thr Leu Glu Glu Arg Pro Phe Val Ile Val Glu Pro			
435	440	445	
GCA GAC CCT ATC AGC GGC ACC TGC ATC CGA GAC TCC GTC CCC TGC CGG		1873	
Ala Asp Pro Ile Ser Gly Thr Cys Ile Arg Asp Ser Val Pro Cys Arg			
450	455	460	
AGC CAG CTC AAC CGA ACC CAC AGC CCT CCA CCG GAT GCC CCC CGC CCG		1921	
Ser Gln Leu Asn Arg Thr His Ser Pro Pro Pro Asp Ala Pro Arg Pro			
465	470	475	
GAA AAG CGC TGC TGC AAG GGT TTC TGC ATC GAC ATT CTG AAG CGG CTG		1969	
Glu Lys Arg Cys Cys Lys Gly Phe Cys Ile Asp Ile Leu Lys Arg Leu			
480	485	490	495
GCG CAT ACC ATC GGC TTC AGC TAC GAC CTC TAC CTG GTC ACC AAT GGC		2017	
Ala His Thr Ile Gly Phe Ser Tyr Asp Leu Tyr Leu Val Thr Asn Gly			
500	505	510	
AAG CAC GGA AAG AAG ATC GAT GGC GTC TGG AAC GGC ATG ATC GGG GAG		2065	
Lys His Gly Lys Lys Ile Asp Gly Val Trp Asn Gly Met Ile Gly Glu			
515	520	525	
GTC TTC TAC CAG CGC GCA GAC ATG GCC ATC GGC TCC CTC ACC ATC AAC		2113	
Val Phe Tyr Gln Arg Ala Asp Met Ala Ile Gly Ser Leu Thr Ile Asn			
530	535	540	
GAG GAG CGC TCC GAG ATC GTG GAC TTC TCC GTC CCC TTC GTG GAG ACC		2161	
Glu Glu Arg Ser Glu Ile Val Asp Phe Ser Val Pro Phe Val Glu Thr			
545	550	555	
GCG ATC AGC GTC ATG GTG GCG CGC AGC AAT GGC ACG GTG TCC CCC TCG		2209	
Gly Ile Ser Val Met Val Ala Arg Ser Asn Gly Thr Val Ser Pro Ser			
560	565	570	575
GCC TTC CTC GAG CCC TAC AGC CCC GCC GTG TGG GTG ATG ATG TTC GTC		2257	
Ala Phe Leu Glu Pro Tyr Ser Pro Ala Val Trp Val Met Met Phe Val			
580	585	590	
ATG TGC CTC ACT GTG GTC GCC GTC ACT GTT TTC ATC TTC GAG TAC CTC		2305	
Met Cys Leu Thr Val Val Ala Val Thr Val Phe Ile Phe Glu Tyr Leu			
595	600	605	
AGT CCT GTT GGT TAC AAC CGC AGC CTG GCC ACG GGC AAG CGC CCT GGC		2353	
Ser Pro Val Gly Tyr Asn Arg Ser Leu Ala Thr Gly Lys Arg Pro Gly			
610	615	620	
GGT TCA ACC TTC ACC ATT GGG AAA TCC ATC TGG CTG CTC TGG GCC CTG		2401	
Gly Ser Thr Phe Thr Ile Gly Lys Ser Ile Trp Leu Leu Trp Ala Leu			
625	630	635	

GTG TTC AAT AAT TCG GTG CCC GTG GAG AAC CCC CGG GGA ACC ACC AGC Val Phe Asn Asn Ser Val Val Pro Glu Asn Pro Arg Gly Thr Thr Ser 640 645 650 655	2449
AAA ATC ATG GTG CTG GTG TGG GCC TTC TTC GCC GTC ATC TTC CTC GCC Lys Ile Met Val Leu Val Trp Ala Phe Phe Ala Val Ile Phe Leu Ala 660 665 670	2497
AGC TAC ACA GCC AAC CTG GCC GCC TTC ATG ATC CAG GAG GAG TAC GTG Ser Tyr Thr Ala Asn Leu Ala Phe Met Ile Gln Glu Glu Tyr Val 675 680 685	2545
GAT ACT GTG TCT GGG CTC AGT GAC CGC AAG TTC CAG AGG CCC CAG GAG Asp Thr Val Ser Gly Leu Ser Asp Arg Lys Phe Gln Arg Pro Gln Glu 690 695 700	2593
CAG TAC CCG CCC CTG AAG TTT GGG ACC GTG CCC AAC GGC TCC ACG GAG Gln Tyr Pro Pro Leu Lys Phe Gly Thr Val Pro Asn Gly Ser Thr Glu 705 710 715	2641
AAG AAC ATC CGC AGC AAC TAT CCC GAC ATG CAC AGC TAC ATG GTG CGC Lys Asn Ile Arg Ser Asn Tyr Pro Asp Met His Ser Tyr Met Val Arg 720 725 730 735	2689
TAC AAC CAG CCC CGC GTA GAG GAA GCG CTC ACT CAG CTC AAG GCA GGG Tyr Asn Gln Pro Arg Val Glu Ala Leu Thr Gln Leu Lys Ala Gly 740 745 750	2737
AAG CTG GAC GCC TTC ATC TAC GAT GCT GCA GTG CTC AAT TAC ATG GCC Lys Leu Asp Ala Phe Ile Tyr Asp Ala Ala Val Leu Asn Tyr Met Ala 755 760 765	2785
CGC AAG GAC GAG GGC TGC AAG CTT GTC ACC ATC GGC TCC GGC AAG GTC Arg Lys Asp Glu Gly Cys Lys Leu Val Thr Ile Gly Ser Gly Lys Val 770 775 780	2833
TTC GCC ACG ACA GGC TAT GGC ATC GCC CTG CAC AAG GGC TCC CGC TGG Phe Ala Thr Thr Gly Tyr Gly Ile Ala Leu His Lys Gly Ser Arg Trp 785 790 795	2881
AAG CGG CCC ATC GAC CTG GCG TTG CTG CAG TTC CTG GGG GAT GAT GAG Lys Arg Pro Ile Asp Leu Ala Leu Leu Gln Phe Leu Gly Asp Asp Glu 800 805 810 815	2929
ATC GAG ATG CTG GAG CGG CTG TGG CTC TCT GGG ATC TGC CAC AAT GAC Ile Glu Met Leu Glu Arg Leu Trp Leu Ser Gly Ile Cys His Asn Asp 820 825 830	2977
AAA ATC GAG GTG ATG AGC AGC AAG CTG GAC ATC GAC AAC ATG GCG GGC Lys Ile Glu Val Met Ser Ser Lys Leu Asp Ile Asp Asn Met Ala Gly 835 840 845	3025
GTC TTC TAC ATG CTC CTG GTG GCC ATG GGC CTG TCC CTG CTG GTC TTS Val Phe Tyr Met Leu Leu Val Ala Met Gly Leu Ser Leu Leu Val Phe 850 855 860	3073
GCC TGG GAG CAC CTG GTG TAC TGG CGC CTG CGG CAC TGC CTG GGG CCC Ala Trp Glu His Leu Val Tyr Trp Arg Leu Arg His Cys Leu Gly Pro 865 870 875	3121
ACC CAC CGC ATG GAC TTC CTG CTG GCC TTC TCC AGG GGC ATG TAC AGC Thr His Arg Met Asp Phe Leu Leu Ala Phe Ser Arg Gly Met Tyr Ser 880 885 890 895	3169
TGC TGC AGC GCT GAG GCC CCA CCG CCC GCC AAG CCC CCG CCG CCC Cys Cys Ser Ala Glu Ala Ala Pro Pro Ala Lys Pro Pro Pro Pro 900 905 910	3217

CCA CAG CCC CTG CCC AGC CCC GCG TAC CCC GCG CCG GGG CCG GCT CCC Pro Gln Pro Leu Pro Ser Pro Ala Tyr Pro Ala Pro Gly Pro Ala Pro 915 920 925	3265
GGG CCC GCA CCT TTC GTC CCC CGC GAG CGC GCC TCA GTG GCC CGC TGG Gly Pro Ala Pro Phe Val Pro Arg Glu Arg Ala Ser Val Ala Arg Trp 930 935 940	3313
CGC CGG CCC AAG GGC GCG GGG CCG CCG GGG GGC GCG GGC CTG GCC GAC Arg Arg Pro Lys Gly Ala Gly Pro Pro Gly Gly Ala Gly Leu Ala Asp 945 950 955	3361
GGC TTC CAC CGC TAC TAC GGC CCC ATC GAG CCG CAG GGC CTA GGC CTC Gly Phe His Arg Tyr Tyr Gly Pro Ile Glu Pro Gln Gly Leu Gly Leu 960 965 970 975	3409
GGC CTG GGC GAA GCG CGC GCG GCA CCG CGG GGC GCA GCC GGG CGC CCG Gly Leu Gly Ala Arg Ala Ala Pro Arg Gly Ala Ala Gly Arg Pro 980 985 990	3457
CTG TCC CCG CCG GCC GCT CAG CCC CCG CAG AAG CCG CCG GCC TCC TAT Leu Ser Pro Pro Ala Ala Gln Pro Pro Gln Lys Pro Pro Ala Ser Tyr 995 1000 1005	3505
TTC GCC ATC GTA CGC GAC AAG GAG CCA GCC GAG CCC CCC GCC GGC GGC Phe Ala Ile Val Arg Asp Lys Glu Pro Ala Glu Pro Pro Ala Gly Ala 1010 1015 1020	3553
TTC CCC GGC TTC CCG TCC CCG CCC GCG CCC CCC GCC GCC GCG GCC ACC Phe Pro Gly Phe Pro Ser Pro Pro Ala Pro Pro Ala Ala Ala Thr 1025 1030 1035	3601
GCC GTC GGG CCG CCA CTC TGC CGC TTG GCC TTC GAG GAC GAG AGC CCG Ala Val Gly Pro Pro Leu Cys Arg Leu Ala Phe Glu Asp Glu Ser Pro 1040 1045 1050 1055	3649
CCG GCG CCC GCG CGG TGG CCG CGC TCG GAC CCC GAG AGC CAA CCC CTG Pro Ala Pro Ala Arg Trp Pro Arg Ser Asp Pro Glu Ser Gln Pro Leu 1060 1065 1070	3697
CTG GGG CCA GGC GCG GGC GCG GGG GGC ACG GGG GGC GCA GGC GGA Leu Gly Pro Gly Ala Gly Gly Ala Gly Gly Thr Gly Ala Gly Gly 1075 1080 1085	3745
GGA GCC CCG GCC GCT CCG CCC CCG TGC TTC GCC GCG CCG CCC CCG TGC Gly Ala Pro Ala Ala Pro Pro Pro Cys Phe Ala Ala Pro Pro Pro Cys 1090 1095 1100	3793
TTT TAC CTC GAT GTC GAC CAG TCG CCG TCG GAC TCG GAG GAC TCG GAG Phe Tyr Leu Asp Val Asp Gln Ser Pro Ser Asp Ser Glu Asp Ser Glu 1105 1110 1115	3841
AGC CTG GCC GGC GCG TCC CTG GCC CTG GAT CCC TGG TGG TTC GCC Ser Leu Ala Gly Ala Ser Leu Ala Gly Leu Asp Pro Trp Trp Phe Ala 1120 1125 1130 1135	3889
GAC TTC CCT TAC CCG TAT GCC GAT CGC CTC GGG CSG CCC GCG GCA CGC Asp Phe Pro Tyr Pro Tyr Ala Asp Arg Leu Gly Xaa Pro Ala Ala Arg 1140 1145 1150	3937
TAC GGA TTG GTC GAC AAA CTA GGG GGC TGG CTC GCC GGG AGC TGG GAC Tyr Gly Leu Val Asp Lys Leu Gly Gly Trp Leu Ala Gly Ser Trp Asp 1155 1160 1165	3985
TAC CTG CCT CCS CGC AGC GGT CGG GCC TGG CAC TGT CGG CAC TGC Tyr Leu Pro Xaa Arg Ser Gly Arg Ala Ala Trp His Cys Arg His Cys 1170 1175 1180	4033

GCC AGC CTG GAG CTG CTT CCG CCG CCG CGC CAT CTC AGC TGC TCG CAC Ala Ser Leu Glu Leu Leu Pro Pro Pro Arg His Leu Ser Cys Ser His 1185 1190 1195	4081
GAT GGC CTG GAC GGC GGC TGG TGG GCG CCA CCG CCT CCA CCC TGG GCC Asp Gly Leu Asp Gly Gly Trp Trp Ala Pro Pro Pro Pro Pro Trp Ala 1200 1205 1210 1215	4129
GCC GGG CCC CTG CCC CGA CGC CGG GCC CGC TGC GGG TGC CCG CGG TCG Ala Gly Pro Leu Pro Arg Arg Ala Arg Cys Gly Cys Pro Arg Ser 1220 1225 1230	4177
CAC CCG CAC CGC CCG CGG GCC TCG CAC CGC ACG CCC GCC GCT GCC GCG His Pro His Arg Pro Arg Ala Ser His Arg Thr Pro Ala Ala Ala 1235 1240 1245	4225
CCC CAC CAC CAC AGG CAC CGG CGC GCC GCT GGG GGC TGG GAC CTC CCG Pro His His Arg His Arg Ala Ala Gly Gly Trp Asp Leu Pro 1250 1255 1260	4273
CCG CCC GCG CCC ACC TCG CGC TCG CTC GAG GAC CTC AGC TCG TGC CCT Pro Pro Ala Pro Thr Ser Arg Ser Leu Glu Asp Leu Ser Ser Cys Pro 1265 1270 1275	4321
CGC GCC CCT GCG CGC AGG CTT ACC GGG CCC TCC CGC CAC GCT CGC Arg Ala Ala Pro Ala Arg Arg Leu Thr Gly Pro Ser Arg His Ala Arg 1280 1285 1290 1295	4369
AGG TGT CCG CAC GCC GCG CAC TGG GGG CCG CCTG CCT ACA GCT TCC Arg Cys Pro His Ala Ala His Trp Gly Pro Pro Leu Pro Thr Ala Ser 1300 1305 1310	4417
CAC CGG AGA CAC CGG GGC GGG GAC CTG GGC ACC CGC AGG GGC TCG GCG His Arg Arg His Arg Gly Gly Asp Leu Gly Thr Arg Arg Gly Ser Ala 1315 1320 1325	4465
CAC TTC TCT AGC CTC GAG TCC GAG GTA TGACGGCGGCC CCGGGGGGCCC His Phe Ser Ser Leu Glu Ser Glu Val 1330 1335	4512
CACCGCCCCC TTGGTCAGCG CAGGCCACGG CCCGAGGGGG CGCCCGCAGT GGACAGGACC	4572
CGCGTGGTT GGGAAAGGAAA GCAGTGGAAC TGGCCGGACC CCGCCTGGAG CAGCGTCCTG	4632
CGCCCCCTGG TTCTGGAGGA ACCGCAAGCC GGAGAGGATT TGGTCCCTCA ACTATCACCC	4692
AGG	4695

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1336 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

Met Arg Gly Ala Gly Gly Pro Arg Gly Pro Arg Gly Pro Ala Lys Met
1 5 10 15

Leu Leu Leu Leu Ala Leu Ala Cys Ala Ser Pro Phe Pro Glu Glu Ala
20 25 30

Pro Gly Pro Gly Gly Ala Gly Gly Pro Gly Gly Leu Gly Gly Ala

35

40

45

Arg Pro Leu Asn Val Ala Leu Val Phe Ser Gly Pro Ala Tyr Ala Ala
50 55 60

Glu Ala Ala Arg Leu Gly Pro Ala Val Ala Ala Val Arg Ser Pro
65 70 75 80

Gly Leu Asp Val Arg Pro Val Ala Leu Val Leu Asn Gly Ser Asp Pro
85 90 95

Arg Ser Leu Val Leu Gln Leu Cys Asp Leu Leu Ser Gly Leu Arg Val
100 105 110

His Gly Val Val Phe Glu Asp Asp Ser Arg Ala Pro Ala Val Ala Pro
115 120 125

Ile Leu Asp Phe Leu Ser Ala Gln Thr Ser Leu Pro Ile Val Ser Glu
130 135 140

His Gly Gly Ala Ala Leu Val Leu Thr Pro Lys Glu Lys Gly Ser Thr
145 150 155 160

Phe Leu His Leu Gly Ser Ser Pro Glu Gln Gln Leu Gln Val Ile Phe
165 170 175

Glu Val Leu Glu Glu Tyr Asp Trp Thr Ser Phe Val Ala Val Thr Thr
180 185 190

Arg Ala Pro Gly His Arg Ala Phe Leu Ser Tyr Ile Glu Val Leu Thr
195 200 205

Asp Gly Ser Leu Val Gly Trp Glu His Arg Gly Ala Leu Thr Leu Asp
210 215 220

Pro Gly Ala Gly Glu Ala Val Leu Ser Ala Gln Leu Arg Ser Val Ser
225 230 235 240

Ala Gln Ile Arg Leu Leu Phe Cys Ala Arg Glu Glu Ala Glu Pro Val
245 250 255

Phe Arg Ala Ala Glu Glu Ala Gly Leu Thr Gly Ser Gly Tyr Val Trp
260 265 270

Phe Met Val Gly Pro Gln Leu Ala Gly Gly Ser Gly Ala Pro
275 280 285

Gly Glu Pro Pro Leu Leu Pro Gly Gly Ala Pro Leu Pro Ala Gly Leu
290 295 300

Phe Ala Val Arg Ser Ala Gly Trp Arg Asp Asp Leu Ala Arg Arg Val
305 310 315 320

Ala Ala Gly Val Ala Val Val Ala Arg Gly Ala Gln Ala Leu Leu Arg
325 330 335

Asp Tyr Gly Phe Leu Pro Glu Leu Gly His Asp Cys Arg Ala Gln Asn
340 345 350

Arg Thr His Arg Gly Glu Ser Leu His Arg Tyr Phe Met Asn Ile Thr
355 360 365

Trp Asp Asn Arg Asp Tyr Ser Phe Asn Glu Asp Gly Phe Leu Val Asn
370 375 380

Pro Ser Leu Val Val Ile Ser Leu Thr Arg Asp Arg Arg Thr Trp Glu Val
385 390 395 400

Val Gly Ser Trp Glu Gln Gln Thr Leu Arg Leu Lys Tyr Pro Leu Trp
415 410 415

Ser Arg Tyr Glu Arg Phe Leu Gln Pro Val Asp Asp Thr Gln His Leu
420 425 430

Ala Val Ala Thr Leu Glu Glu Arg Pro Phe Val Ile Val Glu Pro Ala
435 440 445

Asp Pro Ile Ser Gly Thr Cys Ile Arg Asp Ser Val Pro Cys Arg Ser
450 455 460

Gln Leu Asn Arg Thr His Ser Pro Pro Pro Asp Ala Pro Arg Pro Glu
465 470 475 480

Lys Arg Cys Cys Lys Gly Phe Cys Ile Asp Ile Leu Lys Arg Leu Ala
485 490 495

His Thr Ile Gly Phe Ser Tyr Asp Leu Tyr Leu Val Thr Asn Gly Lys
500 505 510

His Gly Lys Lys Ile Asp Gly Val Trp Asn Gly Met Ile Gly Glu Val
515 520 525

Phe Tyr Gln Arg Ala Asp Met Ala Ile Gly Ser Leu Thr Ile Asn Glu
530 535 540

Glu Arg Ser Glu Ile Val Asp Phe Ser Val Pro Phe Val Glu Thr Gly
545 550 555 560

Ile Ser Val Met Val Ala Arg Ser Asn Gly Thr Val Ser Pro Ser Ala
565 570 575

Phe Leu Glu Pro Tyr Ser Pro Ala Val Trp Val Met Met Phe Val Met
580 585 590

Cys Leu Thr Val Val Ala Val Thr Val Phe Ile Phe Glu Tyr Leu Ser
595 600 605

Pro Val Gly Tyr Asn Arg Ser Leu Ala Thr Gly Lys Arg Pro Gly Gly
610 615 620

Ser Thr Phe Thr Ile Gly Lys Ser Ile Trp Leu Leu Trp Ala Leu Val
625 630 635 640

Phe Asn Asn Ser Val Pro Val Glu Asn Pro Arg Gly Thr Thr Ser Lys
645 650 655

Ile Met Val Leu Val Trp Ala Phe Phe Ala Val Ile Phe Leu Ala Ser
660 665 670

Tyr Thr Ala Asn Leu Ala Ala Phe Met Ile Gln Glu Glu Tyr Val Asp
675 680 685

Thr Val Ser Gly Leu Ser Asp Arg Lys Phe Gln Arg Pro Gln Glu Gln
690 695 700

Tyr Pro Pro Leu Lys Phe Gly Thr Val Pro Asn Gly Ser Thr Glu Lys
705 710 715 720

Asn Ile Arg Ser Asn Tyr Pro Asp Met His Ser Tyr Met Val Arg Tyr
725 730 735

Asn Gln Pro Arg Val Glu Glu Ala Leu Thr Gln Leu Lys Ala Gly Lys
740 745 750

Leu Asp Ala Phe Ile Tyr Asp Ala Ala Val Leu Asn Tyr Met Ala Arg

755	760	765
Lys Asp Glu Gly Cys Lys Leu Val Thr Ile Gly Ser Gly Lys Val Phe		
770	775	780
Ala Thr Thr Gly Tyr Gly Ile Ala Leu His Lys Gly Ser Arg Trp Lys		
785	790	795
Arg Pro Ile Asp Leu Ala Leu Gln Phe Leu Gly Asp Asp Glu Ile		
805	810	815
Glu Met Leu Glu Arg Leu Trp Leu Ser Gly Ile Cys His Asn Asp Lys		
820	825	830
Ile Glu Val Met Ser Ser Lys Leu Asp Ile Asp Asn Met Ala Gly Val		
835	840	845
Phe Tyr Met Leu Leu Val Ala Met Gly Leu Ser Leu Leu Val Phe Ala		
850	855	860
Trp Glu His Leu Val Tyr Trp Arg Leu Arg His Cys Leu Gly Pro Thr		
865	870	875
880		
His Arg Met Asp Phe Leu Leu Ala Phe Ser Arg Gly Met Tyr Ser Cys		
885	890	895
Cys Ser Ala Glu Ala Ala Pro Pro Ala Lys Pro Pro Pro Pro		
900	905	910
Gln Pro Leu Pro Ser Pro Ala Tyr Pro Ala Pro Gly Pro Ala Pro Gly		
915	920	925
Pro Ala Pro Phe Val Pro Arg Glu Arg Ala Ser Val Ala Arg Trp Arg		
930	935	940
Arg Pro Lys Gly Ala Gly Pro Pro Gly Gly Ala Gly Leu Ala Asp Gly		
945	950	955
960		
Phe His Arg Tyr Tyr Gly Pro Ile Glu Pro Gln Gly Leu Gly Leu Gly		
965	970	975
Leu Gly Glu Ala Arg Ala Ala Pro Arg Gly Ala Ala Gly Arg Pro Leu		
980	985	990
Ser Pro Pro Ala Ala Gln Pro Pro Gln Lys Pro Pro Ala Ser Tyr Phe		
995	1000	1005
Ala Ile Val Arg Asp Lys Glu Pro Ala Glu Pro Pro Ala Gly Ala Phe		
1010	1015	1020
Pro Gly Phe Pro Ser Pro Pro Ala Pro Pro Ala Ala Ala Ala Thr Ala		
1025	1030	1035
1040		
Val Gly Pro Pro Leu Cys Arg Leu Ala Phe Glu Asp Glu Ser Pro Pro		
1045	1050	1055
Ala Pro Ala Arg Trp Pro Arg Ser Asp Pro Glu Ser Gln Pro Leu Leu		
1060	1065	1070
Gly Pro Gly Ala Gly Gly Ala Gly Gly Thr Gly Gly Ala Gly Gly Gly		
1075	1080	1085
Ala Pro Ala Ala Pro Pro Cys Phe Ala Ala Pro Pro Pro Cys Phe		
1090	1095	1100
Tyr Leu Asp Val Asp Gln Ser Pro Ser Asp Ser Glu Asp Ser Glu Ser		
1105	1110	1115
1120		

Leu Ala Gly Ala Ser Leu Ala Gly Leu Asp Pro Trp Trp Phe Ala Asp
1125 1130 1135

Phe Pro Tyr Pro Tyr Ala Asp Arg Leu Gly Xaa Pro Ala Ala Arg Tyr
1140 1145 1150

Gly Leu Val Asp Lys Leu Gly Gly Trp Leu Ala Gly Ser Trp Asp Tyr
1155 1160 1165

Leu Pro Xaa Arg Ser Gly Arg Ala Ala Trp His Cys Arg His Cys Ala
1170 1175 1180

Ser Leu Glu Leu Leu Pro Pro Pro Arg His Leu Ser Cys Ser His Asp
1185 1190 1195 1200

Gly Leu Asp Gly Gly Trp Trp Ala Pro Pro Pro Pro Trp Ala Ala
1205 1210 1215

Gly Pro Leu Pro Arg Arg Ala Arg Cys Gly Cys Pro Arg Ser His
1220 1225 1230

Pro His Arg Pro Arg Ala Ser His Arg Thr Pro Ala Ala Ala Pro
1235 1240 1245

His His His Arg His Arg Arg Ala Ala Gly Gly Trp Asp Leu Pro Pro
1250 1255 1260

Pro Ala Pro Thr Ser Arg Ser Leu Glu Asp Leu Ser Ser Cys Pro Arg
1265 1270 1275 1280

Ala Ala Pro Ala Arg Arg Leu Thr Gly Pro Ser Arg His Ala Arg Arg
1285 1290 1295

Cys Pro His Ala Ala His Trp Gly Pro Pro Leu Pro Thr Ala Ser His
1300 1305 1310

Arg Arg His Arg Gly Gly Asp Leu Gly Thr Arg Arg Gly Ser Ala His
1315 1320 1325

Phe Ser Ser Leu Glu Ser Glu Val
1330 1335

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 71 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

GGGTGGCGGC CGCAGAGCAC CTCCACCATC TCCTTGTGCT ACTCCAAGAT CTGGCCCTAG 60
TCCATGTTTG C 71

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 71 base pairs
(B) TYPE: nucleic acid

- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

TGGTGGTCCC CAACCTGTAG GACTTGGTTC TGGAGGAGGA TCTGGTAG GC	60
ACTAGGGCCA G	71

(2) INFORMATION FOR SEQ ID NO:61:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 61 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

GTTGGGGACC ACCAGATGGA GGTAGAGCTG CACTTGTACG AAGAGCTCCA CAACCACCTG	60
G	61

(2) INFORMATION FOR SEQ ID NO:62:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 62 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

CGTGAGACGT CAGACAAAGG AGGCCAGGT GTAGGTGGTC TACCAAGGTG TTGTGGAGCT	60
CT	62

(2) INFORMATION FOR SEQ ID NO:63:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 195 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

CCGCAGAGCA CCTCCACCAT CTCTTGTC TACTCCAAGA TCTGGCCCTA GTCCATGTTT	60
GCCTACACCA GATCCTCCTC CAGAACCAAG TCCTACAGGT TGGGGACAC CAGATGGAGG	120
TAGAGCTGCA CTTGTACGAA GAGCTCCACA ACCACCTGGT AGACCACCTA CACCTGGCC	180
TCCTTTGTCT GACGT	195